

**Figure 1a**

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**(SEQ ID 147)**

**Figure 1b**

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**(SEQ ID 148)**

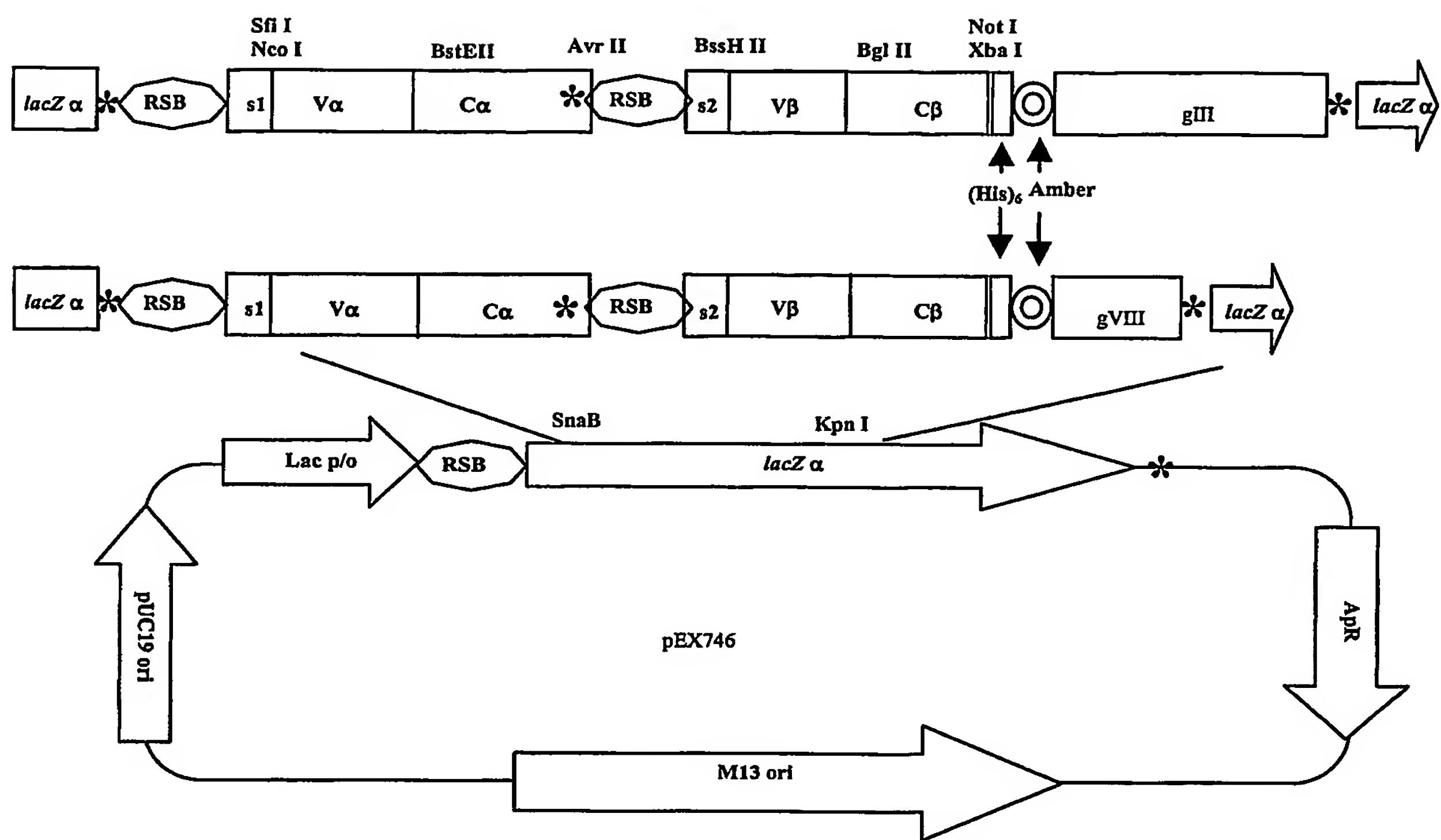
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PESS\*  
**(SEQ ID 149)**

**Figure 2b**

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**(SEQ ID 150)**

Figure 3



**Figure 4**

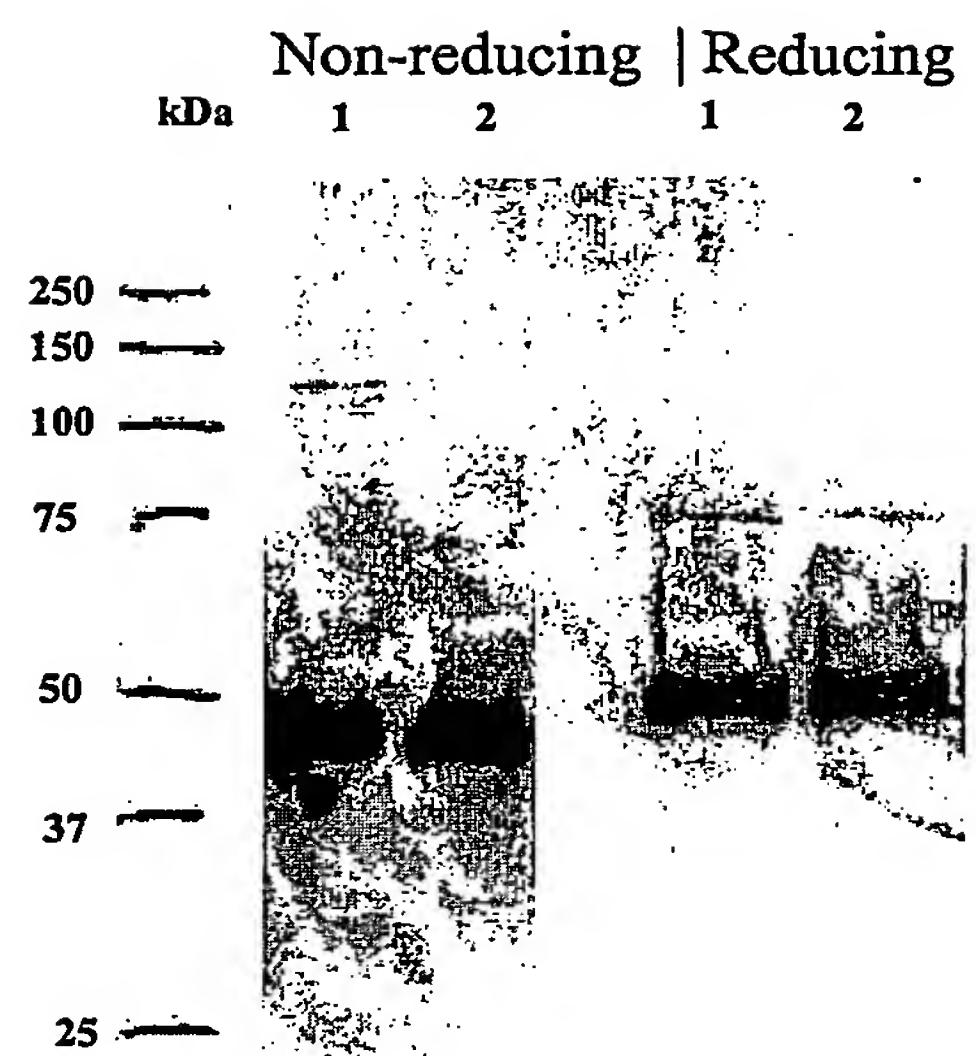
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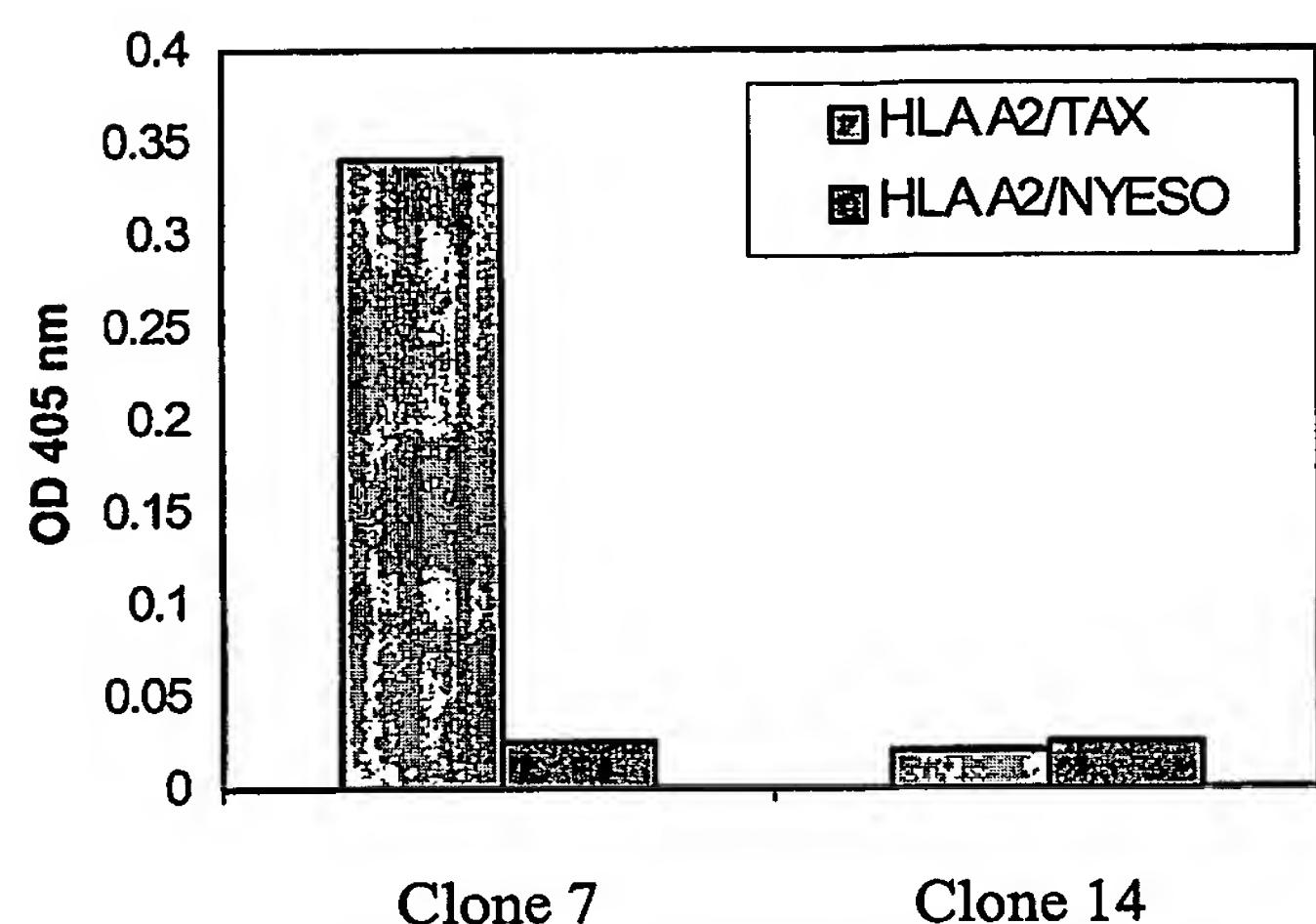
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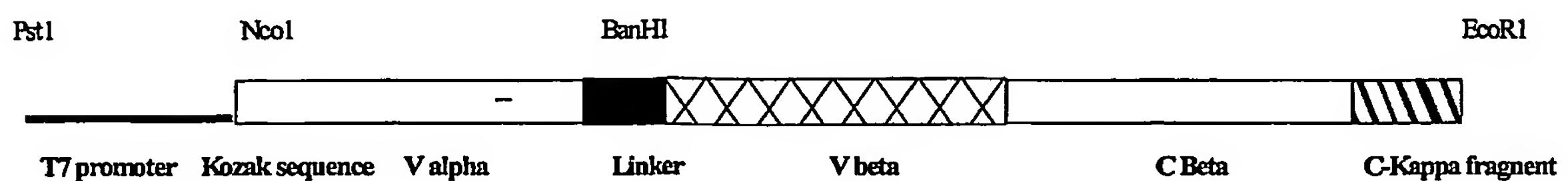
**(SEQ ID 151)**

**Figure 5**

**Figure 6**

**Figure 7a**

## Schematic diagram of the A6 scTCR-C-Kappa ribosome display construct



**Figure 7b**

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**(SEQ ID 152)**

**Figure 7C**

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E	S																				

**(SEQ ID: 153)**

**Figure 8****pUC19-T7 sequence**

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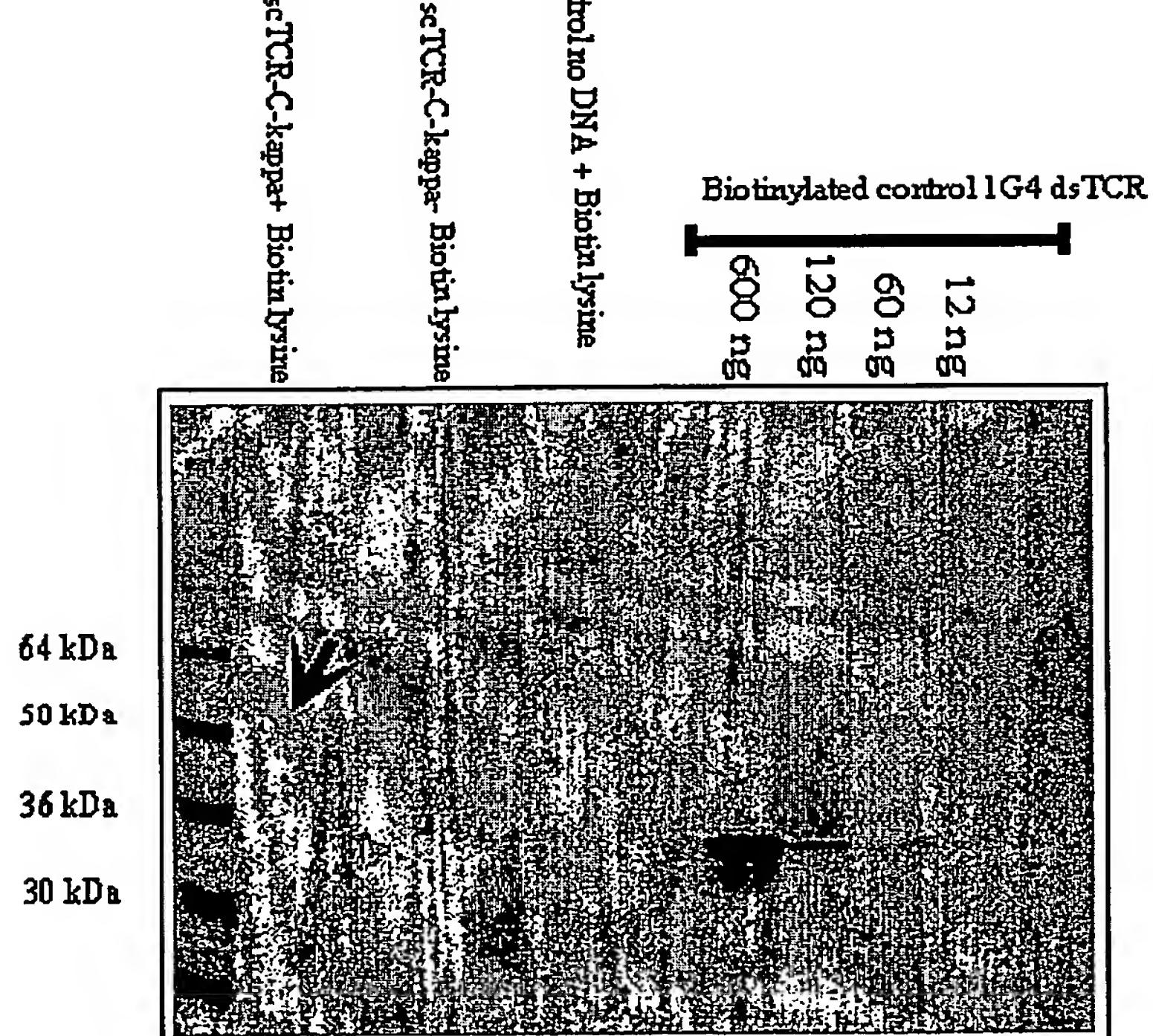
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**(SEQ ID 154)**

**Figure 9****A6 scTCR-C-kappa cloned into pUC19-T7**

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101 gtccttcttc tggtacagac aatattctgg gaaaagccct gagttataa  
151 tgcctatata ctccaatggt gacaaagaag atggaagggt tacagcacag  
201 ctcaataaaag ccagccagta tggttctctg ctcatcagag actcccagcc  
251 cagtgattca gccacctacc tctgtccgt tacaactgac agctggggga  
301 aattgcagtt tggagcaggg acccaggtt tggtcaccgg tggaggcggt  
351 tcaggcggag gtggatccgg cggggcggg tcgaacgctg gtgtcactca  
401 gaccccaaaa ttccaggtcc tgaagacagg acagagcatg acactgcagt  
451 gtgcccagga tatgaaccat gaatacatgt cctggatcgt acaagaccga  
501 ggcattggggc tgaggctgtat tcattactca gttgggtctg gtatcactga  
551 ccaaggagaa gtcccaatgt gctacaatgt ctccagatca accacagagg  
601 atttcccgct caggtgtctg tcggctgtc cctccagac atctgtgtac  
651 ttctgtgcca gcaggccggg actagccgg gggcgaccag agcagtactt  
701 cgggcccgggc accaggctca cggtcacaga ggacctgaaa aacgtgttcc  
751 caccggaggt cgctgtgttt gagccatcag aagcagagat ctcccacacc  
801 caaaaaggcca cactgggtgtg cctggccaca ggcttctacc ccgaccacgt  
851 ggagctgagc tggtgggtga atgggaagga ggtgcacagt ggggtcagca  
901 cagacccgca gcccctcaag gaggcccg ccctcaatga ctcagatac  
951 gctctgagca gccgcctgag ggtctggcc accttctggc aggacccccc  
1001 caaccacttc cgctgtcaag tccagttcta cgggctctcg gagaatgacg  
1051 agtggaccca ggataggggcc aaacccgtca cccagatcg cagcgccgag  
1101 gcctgggtt gaggcagacgg tggaggcggt tcaactcagca gcaccctgac  
1151 gctgagcaaa gcagactacg agaaacacaa agtctacgcc tgcaagtca  
1201 cccatcaggg cctgagttcg cccgtcacaa agagcttcaa cgcggagag  
1251 tcataagaat tc

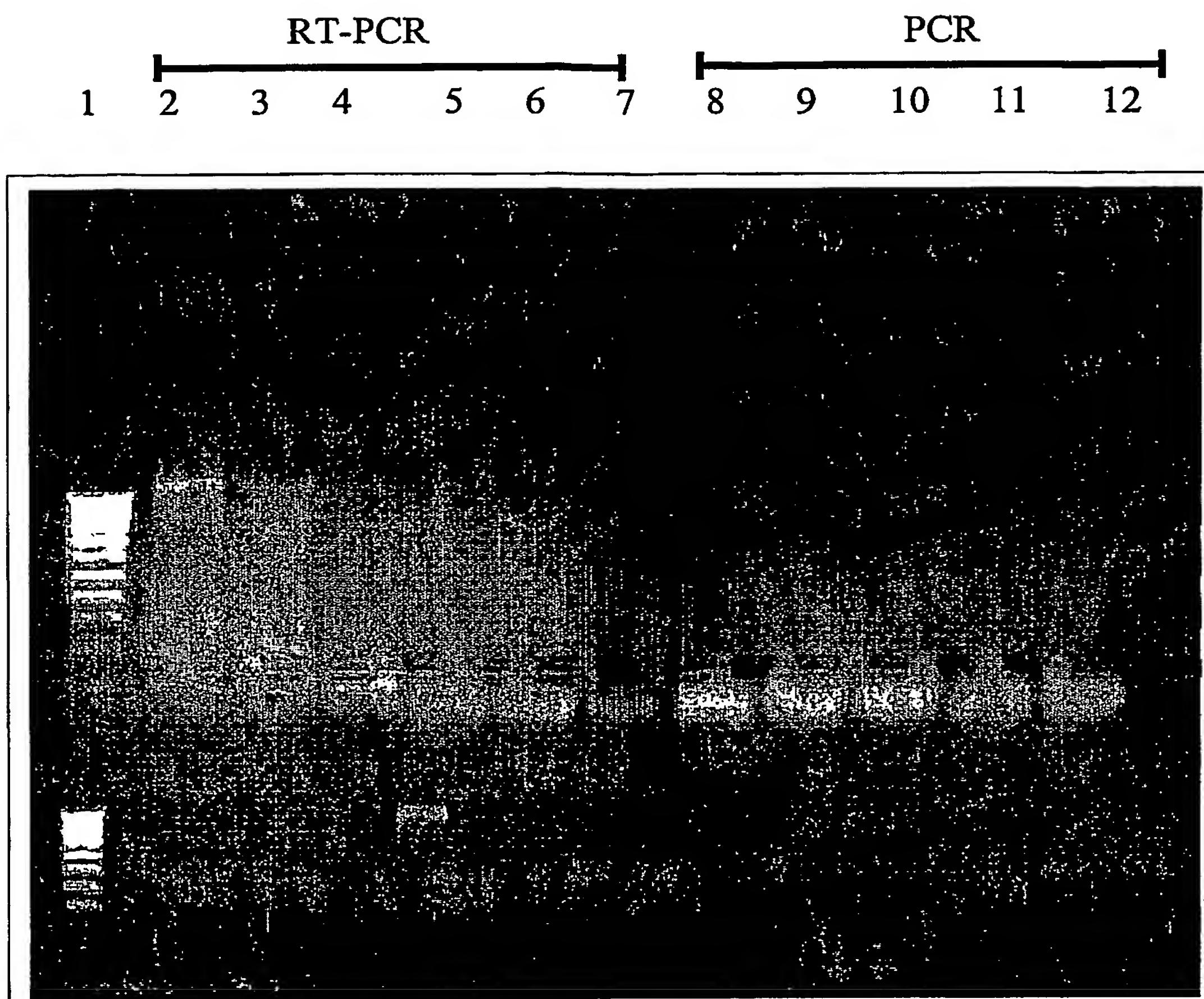
**(SEQ ID 155)**

**Figure 10**

The A6 scTCR-C-Kappa protein is shown in the above western blot with an arrow.

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Figure 11



13 14

15

Lane 1 Bioline 100bp DNA marker

Lane 2 A6scTCR-C-Kappa reaction selected against HLA-A2 TAX beads

Lane 3 A6scTCR-C-Kappa reaction selected against HLA-A2 TAX beads in the presence of 10 microgrammes of soluble A6scTCR

Lane 4 A6scTCR-C-Kappa reaction selected against control beads

Lane 5 Control no DNA reaction selected against HLA-A2-TAX beads

Lane 6 Control no DNA reaction selected against HLA-A2 TAX beads in the presence of 10 microgrammes of soluble A6scTCR

Lane 7 Control no DNA reaction selected against control beads

Lanes 8-12 and lane 13 are as lanes 2-7 except no reverse transcriptase was added just Roche high fidelity taq. These are the DNA contamination controls.

Lane 13 RT-PCR positive control.

**Figure 12a**Clone 9 Mutated A6 TCR  $\beta$  chain DNA sequence

gctgggtcactcagacccaaaattccaggcctgaagacaggacagacactgcagtgtgccaggatataaccat  
gaatacatgtcctggtatcgacaagacccaggcatggggctgaggctgattcattactcagttggctggatcactgaccaagga  
gaagtccccatggctacaatgtctccagatcaaccacagaggattcccgctcaggctgctgcggctgtccctccagacatct  
gtgtacttctgtgccagcaggccggactagccggagggtgaccagagcagacttcggccggcaccaggctacggcac  
agaggacctgaaaaacgtttccacccgaggtcgctgtttgagccatcagaaggcagatctccacacccaaaaggcca  
cactgggtgcctggccacaggcttctaccccgaccacgtggagctgagctgggtgaatggaaaggaggtgcacagtggg  
tctgcacagaccccgagccctcaaggagcagcccccctcaatgactccagatacgctctgagcagccgcctgagggtctcg  
ccaccttctggcaggaccccgcaaccacttcgctgtcaagtccagttctacggctctcgagaaatgacgagtgacccagga  
tagggccaaaccgtcaccagatcgtcagcggcaggcctgggttagagcagac

**(SEQ ID 156)****Figure 12b**Clone 9 Mutated A6 TCR  $\beta$  chain amino acid sequence

AGVTQTPKFQVLKTGQSMLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVP  
NGYNVSRSTTEDFPLRLLSAAPSQTSVYFCASRPGLAGGXPEQYFGPGTRLTVTEDLKNVF  
PPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEVHSGVCTDPQPLKEQPA  
LNDSRYALSSRLRVSATFWQDPRNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEWGR  
AD

**(SEQ ID 157)**

X - Denotes the position of the amino acid corresponding to the introduced 'opal' stop codon, this will generally result in the substitution of a tryptophan (W) residue into the TCR  $\beta$  chain at this point.

**Figure 13****Clone 49 Mutated A6 TCR  $\beta$  chain DNA sequence**

gctggtgtcaactcagacccaaaattccaggtcctgaagacaggacagagcatgacactgttagtgtgccaggatataaccat  
gaatacatgtcctggtatcgacaagacccaggcatggggctgaggctgattcattactcagttggctggtatcactgaccaagga  
gaagtccccatggctacaatgtctccagatcaaccacagaggattcccgctcaggctgctgtcggtctccctccagacatct  
gtgtacttctgtgccagcaggccggactagcgggagggcaccagagcagacttcggccggcaccaggctacggcac  
agaggacctgaaaaacgtgttcccacccgaggtcgctgtttgagccatcagaagcagagatctcccacacccaaaaggcca  
cactggtgtgcctggccacaggcttctacccgaccacgtggagctgagctgggtgaatggaaaggaggtgcacagtgggg  
tctgcacagaccccgagccctcaaggagcagccgcccctcaatgactccagatacgctctgagcagccgcctgagggtctcg  
ccacccctctggcaggaccccgcaaccacttccgtcaagtccagttctacggctctggagaatgacgagtgacccagga  
tagggccaaaccgtcacccagatcgtcagcgccgaggcctgggttagagcagac

**(SEQ ID 158)**

**Figure 14a**

Clone 134 Mutated A6 TCR  $\beta$  chain DNA sequence

gctgggtcactcagacccaaaattccaggcctgaagacagaggacagacactgcagtgtgccaggatataaccat  
gaatacatgtcctggtatcgacaagacccaggcatggggctgaggctgattcattactcagttggctgttatcactgaccaagga  
gaagtccccaaatggctacaatgtctccagatcaaccacagaggattcccgctcaggctgctcggtctccctccagacatct  
gtgtacttctgtgcctcgaggccgggctgtatgagtgcggaaaccagagcagtactcggccggcaccaggctacggtcac  
agaggacatgaaaaacgtttccaccggctgttcggatcggcgttgcggatcggatcggatcggatcggatcggatcggatc  
cactgggtgcctggccaccggttctaccccgaccacgtggagctgagctggatggatggatggatggatggatggatggatc  
ctgcacagaccccgagccctcaaggagcagccgcctcaatgactccagatacgctctgagcagccgcctgagggtctcg  
ccacccctggcaggaccggcaaccacttccgtcaagtccagttctacggctctcgagaatgacgagtgacactgacacc  
tagggccaaaccgtcaccagatcgtagcggcggctgggttagagcagactaagctgaattc  
**(SEQ ID 159)**

**Figure 14b**

Clone 134A Mutated A6 TCR  $\beta$  chain amino acid sequence (BIACore)

MNAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQG  
EVPNGYNVSRSTTEDFPLRLLSAAPSQTSVYFCASRPGLMSAEPEQYFGPGTRLTVTEDLK  
NVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVVELSWWVNGKEVHSGVCTDPQPLKE  
QPALNDSRYALSSRLRVSATFWQDPRNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEA  
WGRAD\*

**(SEQ ID 160)**

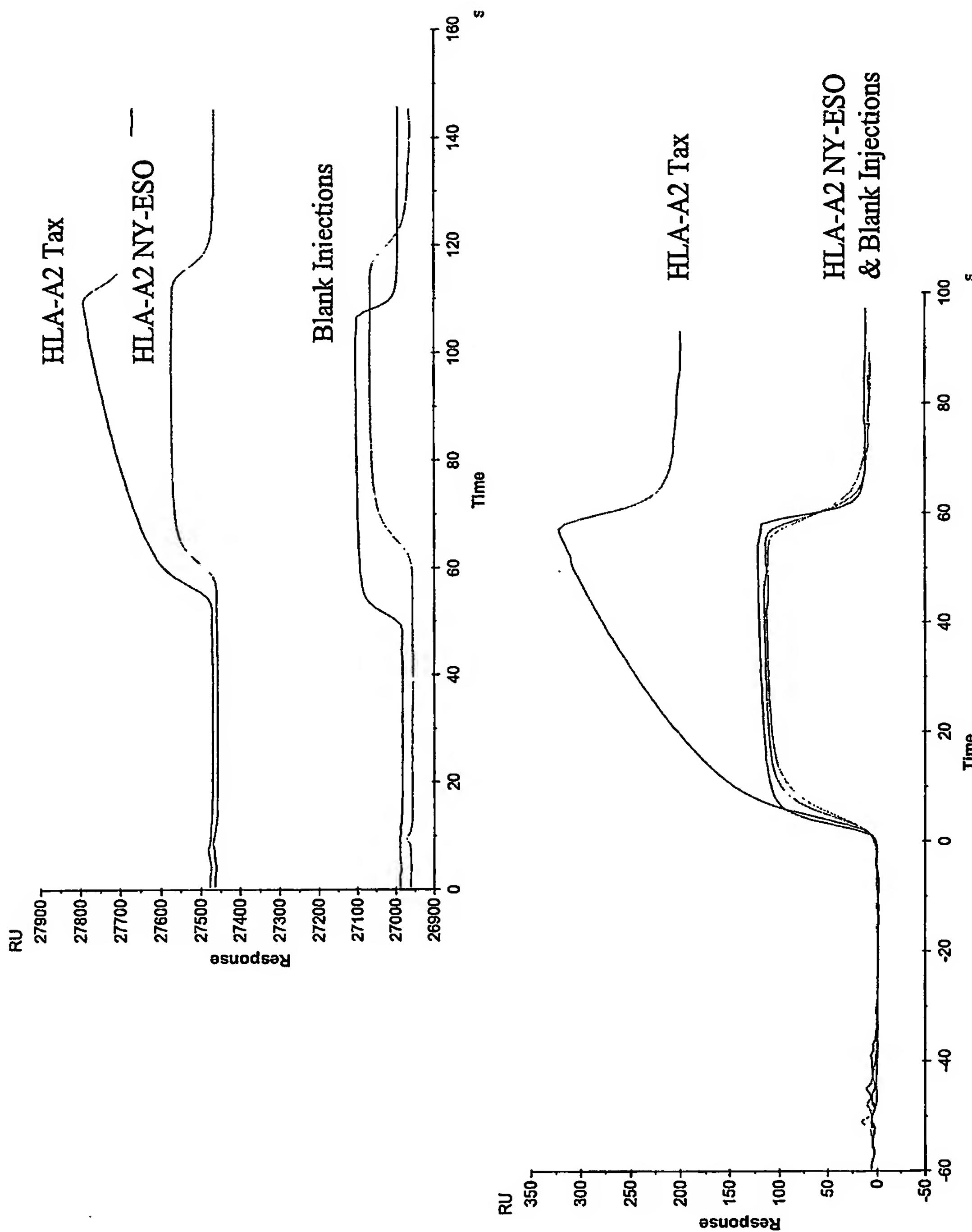
**Figure 14c**

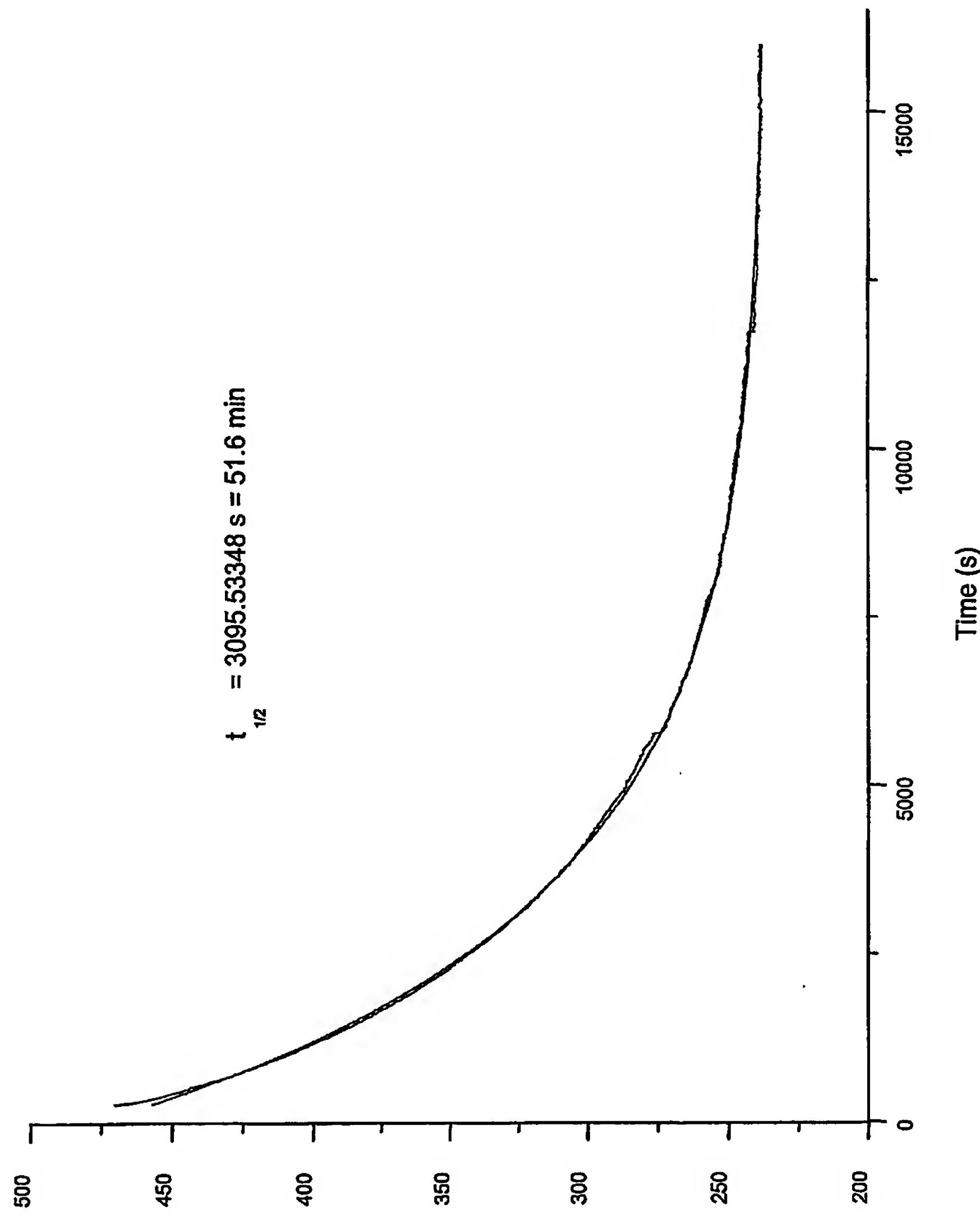
Clone 134 Mutated A6 TCR  $\beta$  chain amino acid sequence (ELISA)

AGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVP  
NGYNVSRSTTEDFPLRLLSAAPSQTSVYFCASRPGLMSAQPEQYFGPGTRLTVTEDLKNVF  
PPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVVELSWWVNGKEVHSGVCTDPQPLKEQPA  
LNDSRYALSSRLRVSATFWQDPRNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEWGR  
AD

**(SEQ ID 161)**

A6 TCR clone 134



**Figure 16**

**Figure 17a**

atgcaggaggacacagattcctgcagctctgagtgtcccagaaggagaaaactggttcaactgcagttcactgata  
 gcgctattacaacccatggtttaggcaggaccctggaaaggctcacatctgttgcatttcaagtcaagtcagaga  
 gagcaaaacaagtggaaagacttaatgcctcgctggataaatcatcaggacgtactttatacattgcagttcagcctgg  
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 gcattattccagaagacacccttccccagcccagaaagttctaa  
**(SEQ ID 162)**

**Figure 17b**

atgggtgtcactcagacccaaaattccaggcctgaagacagggacagacatgacactgcagtgtgcccaggatgaa  
 ccatgaatacatgtcctggatcgacaagacccaggcatgggctgaggctgattcattactcagttggctggatctactg  
 accaaggagaagtccccatggctacaatgtctccagatcaaccacagaggattcccgcctcaggctgctgcccgtc  
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 cagccgcctgagggctcgccacccctggcaggacccttccgcgtcaagtccagttctacggctctc  
 ggagaatgacgagtgacccaggataggccaaacccgtcaccagatgtcagcgccgaggcctgggttagagcag  
 actaa  
**(SEQ ID 163)**

**Figure 18a**

M Q E V T Q I P A A L S V P E G E N L V L N C S F T D S A I Y N L Q W F R Q  
 D P G K G L T S L L I Q S S Q R E Q T S G R L N A S L D K S S G R S T L Y I  
 A A S Q P G D S A T Y L C A V R P T S G G S Y I P T F G R G T S L I V H P Y I  
 Q N P D P A V Y Q L R D S K S S D K S V C L F T D F D S Q T N V S Q S K D S  
 D V Y I T D K C V L D M R S M D F K S N S A V A W S N K S D F A C A N A F  
 N N S I I P E D T F F P S P E S S Stop  
**(SEQ ID 164)**

**Figure 18b**

M G V T Q T P K F Q V L K T G Q S M T L Q C A Q D M N H E Y M S W Y R Q  
 D P G M G L R L I H Y S V G A G I T D Q G E V P N G Y N V S R S T T E D F P  
 L R L L S A A P S Q T S V Y F C A S S Y V G N T G E L F F G E G S R L T V L E  
 D L K N V F P P E V A V F E P S E A E I S H T Q K A T L V C L A T G F Y P D H  
 V E L S W W V N G K E V H S G V C T D P Q P L K E Q P A L N D S R Y A L S  
 S R L R V S A T F W Q D P R N H F R C Q V Q F Y G L S E N D E W T Q D R A  
 K P V T Q I V S A E A W G R A D Stop **(SEQ ID 165)**

Figure 19a

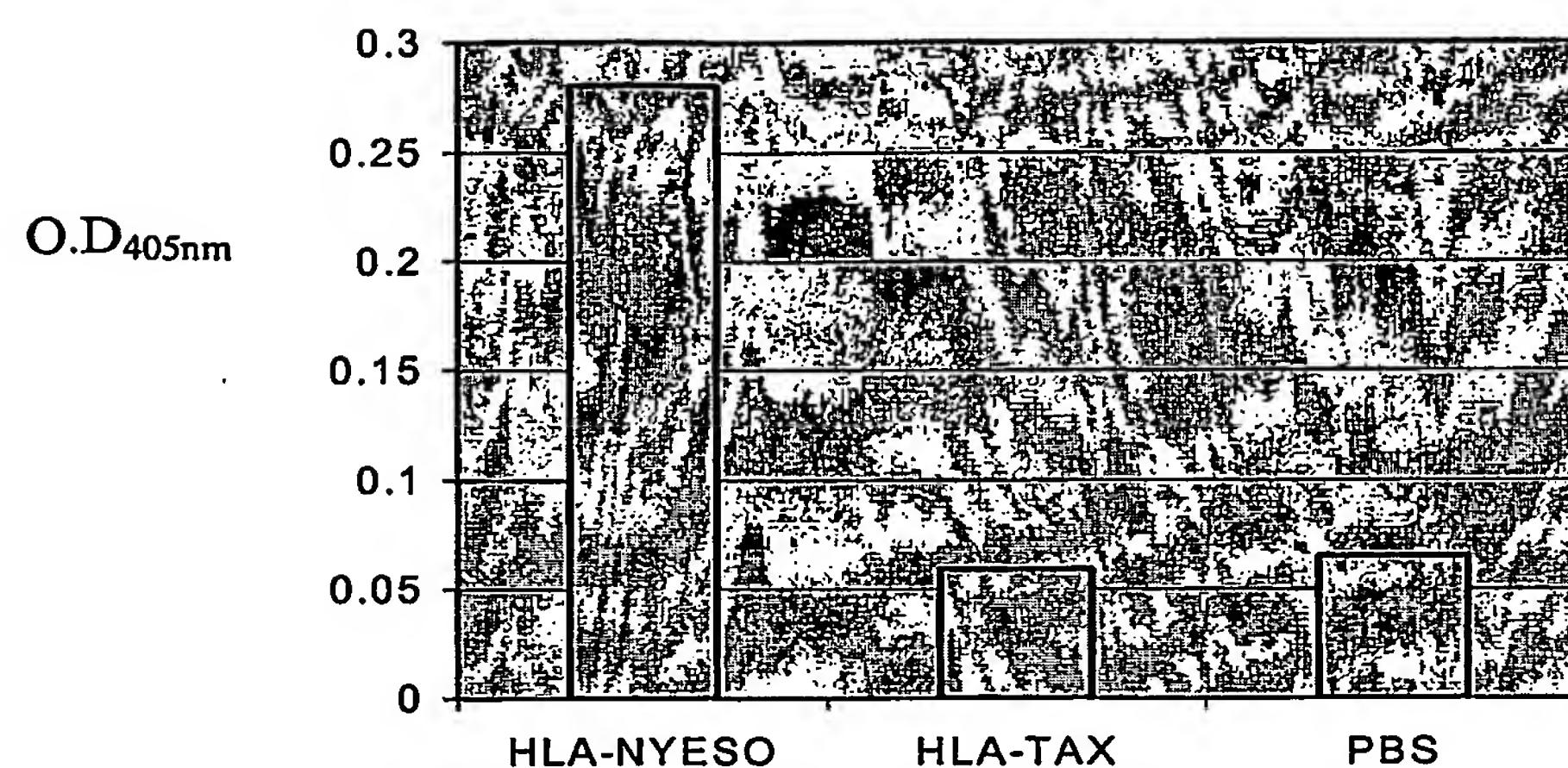
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 TGAATTACGG AGCGACCTAT TTAGTAGTCC TGCACTCATGA AATATGTAAC  
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 TTATTCGCAA TTCCTTGTG TGTCCTTTC TATTCTCACA GCGCGCAGGC  
 AATAAGCGTT AAGGAAATCA ACAAGGAAAG ATAAGAGTGT CGCGCGTCCG  
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 ACCACAGTGA GTCTGGGGTT TTAAGGTCCA GGACTCTGT CCTGTCTCGT  
 TGACACTGCA GTGTGCCAG GATATGAACC ATGAATACAT GTCTGGTAT  
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 CGACAAGACC CAGGCATGGG GCTGAGGCTG ATTCAATTACT CAGTTGGTGC  
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 TGGTATCACT GACCAAGGAG AAGTCCCCAA TGGCTACAAT GTCTCCAGAT  
 ACCATAGTGA CTGGTTCCCTC TTCAGGGGTT ACCGATGTTA CAGAGGTCTA  
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 TGTTCCCACC CGAGGTCGCT GTTGTGAGC CATCAGAACG AGAGATCTCC  
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 TCTATGCGAG ACTCGTCGGC GGACTCCCAG AGCCGGTGGA AGACCGTCCT  
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 GGGGGCGTTG GTGAAGGCCA CAGTCAGGT CAAGATGCC GAGAGCCTCT  
 ATGACGGAGTG GACCCAGGAT AGGGCCAAAC CCGTCACCCA GATCGTCAGC  
 TACTGCTCAC CTGGGTCTA TCCCGGTTTG GGCAGTGGGT CTAGCAGTCG  
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(SEQ ID 166)

**Figure 19b**

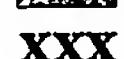
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L L A L S G I P C D S F M A S R H E F S V C G P T L V  
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L A D T N Q S Q S D F N S H G W A T V E V L V E S Y Q  
L P T L S G H K K D A E S T S G S S G E T W K V F T  
G I F G R A G Y D S M C P Y K M V R T F P A W L R Q V  
A Q S K G A S P S Q S A S F L Y S S Q F P K S P L V P  
A T C G S H T H S S R F P P V E Y V S L F Q L Q R Q V  
A V N P T Y P V K V M D F V Q H H N P E V T E P S C A  
T E L D Q L R H S N D S F V F N H Y A G N H V D S R R  
P Q V Q E T V L D T L K M L G A T K S H T L D C A H Q  
L K L R R S A S R Q V N D P D R N S N L H D C A H Q  
L A N F Q R C T L S C S E H T Q L P L G D E P V Y N T  
Y M E W S G L G Q D K W P A Q A G V L V E A Y G R R  
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(SEQ ID 167)

**Figure 20**

**Figure 21****DRA0101**

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121 ctgaatccctg accaatcagg cgagtttatg tttgactttt atgggtatga gattttccat  
181 gtggatatgg caaagaagga gacggctctgg cggcttgaag aatttggacg atttgccagc  
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301 acaaaggcgct ccaactatac tccgatcacc aatgtaccc cagaggtAAC tgtgctcagc  
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421 ccaccaggctt tcaatgtcac gtggcttcga aatggaaaac ctgtcaccac aggagtgtca  
481 gagacagtct tcctgcccag ggaagaccac ctttccgca agttccacta tctcccttc  
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721 gcaatccatgg gatctgggtgg tggctgaac gatattttt aagctcagaa aatcgaatgg  
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841 catgagtagg atcc

**(SEQ ID 168)****Fos Leucine zipper codons****Biotinylation tag codons**

**Figure 22**

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121 taaaagattc taatctgata tgaaaaaaa caccttgcg gcccagttg tttgcgtacg  
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601 ttaacaaaata ctttatccta tttcaaaatt gttgcgttc ttccagcgaa ccaaaactat  
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9961 cgcaacgcgtt gttaggccac cacttcaaga actctgttagc accgcctaca

10021 cttccggctc gtatgttgc tggaattgtg agcggataac aatttcacac aggaaacagc  
10081 tatgaccatg attacg

**(SEQ ID 169)**



- Restriction enzyme sites

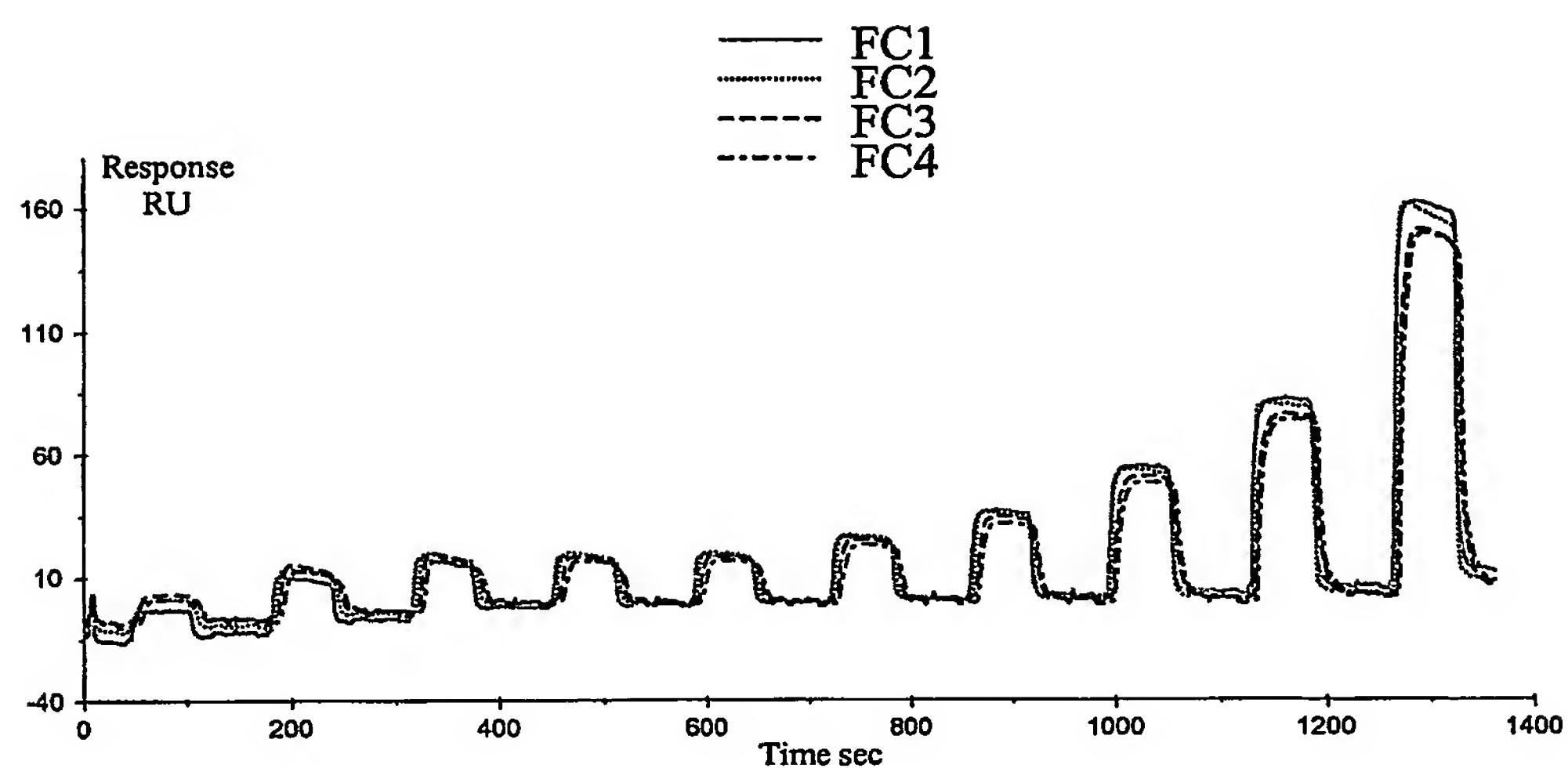
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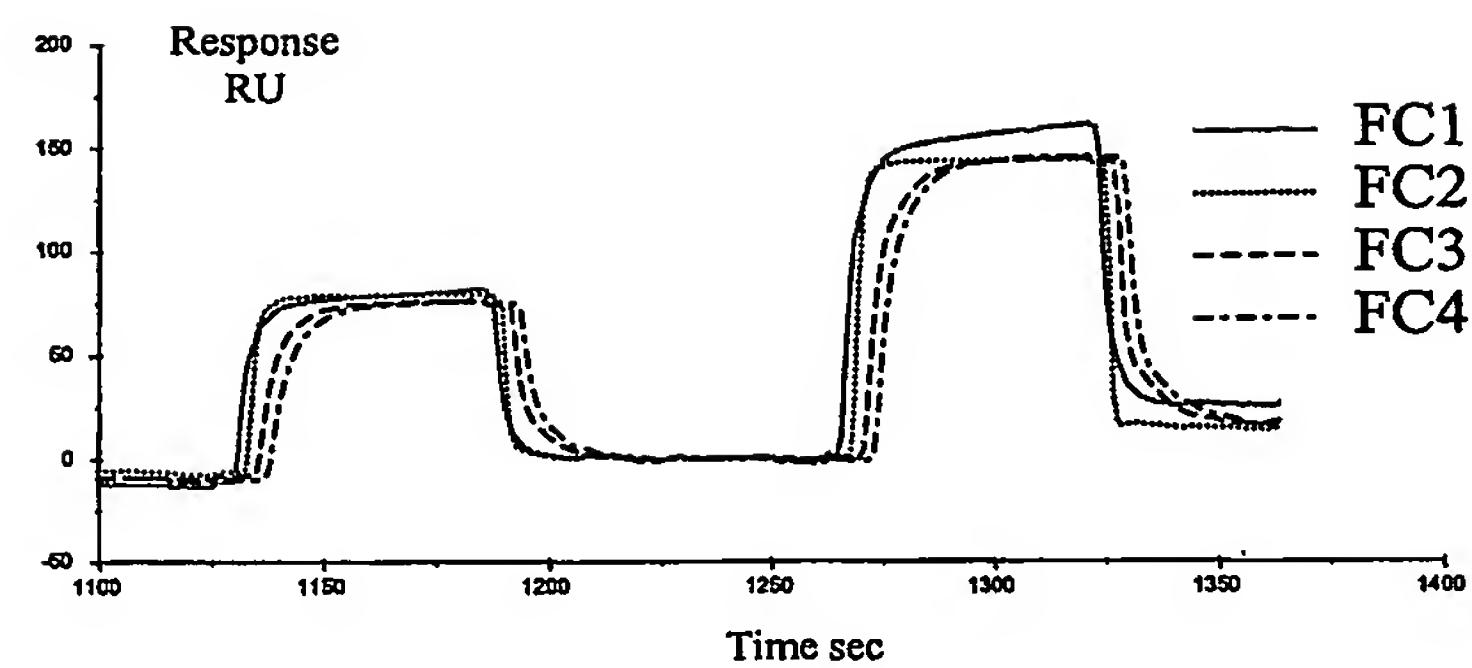
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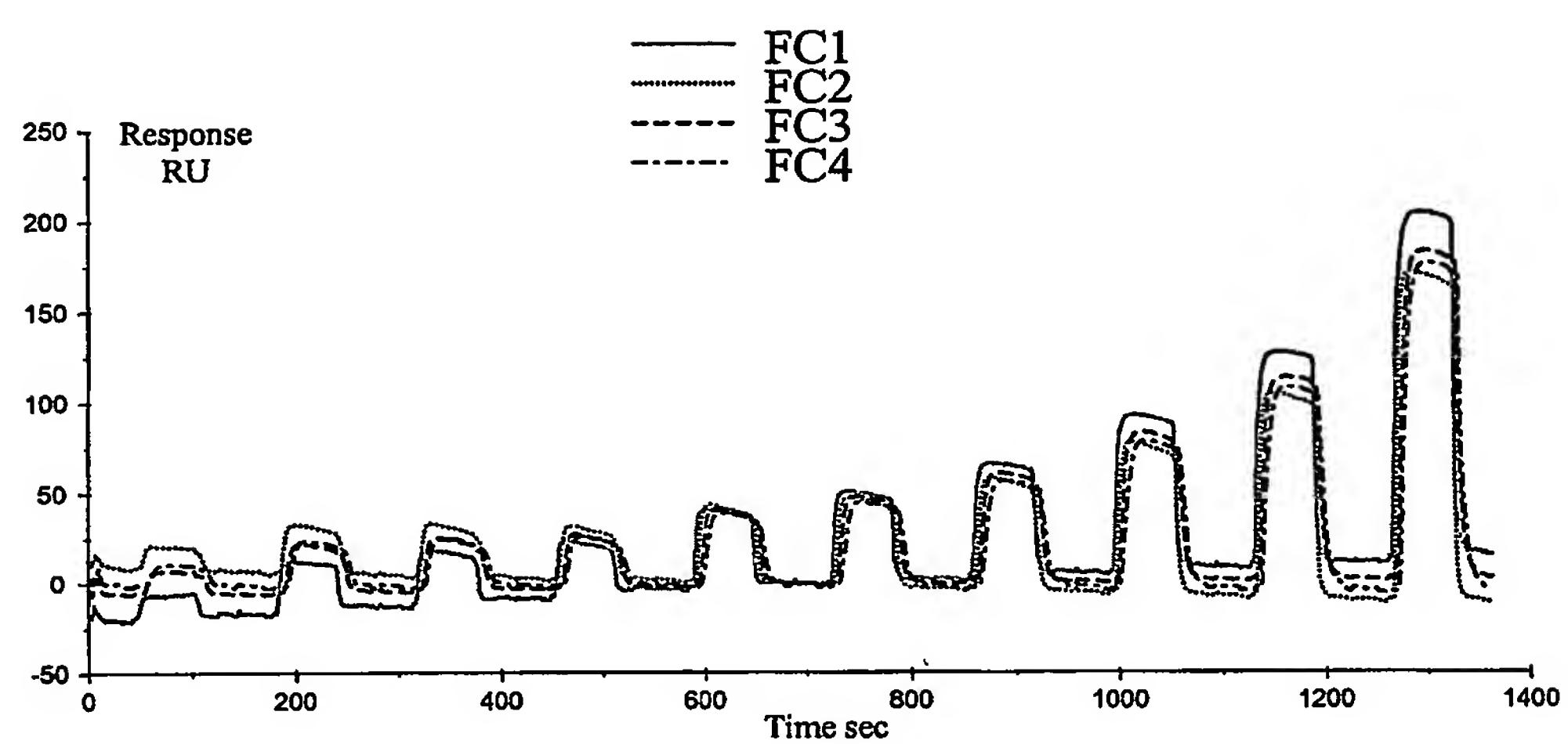
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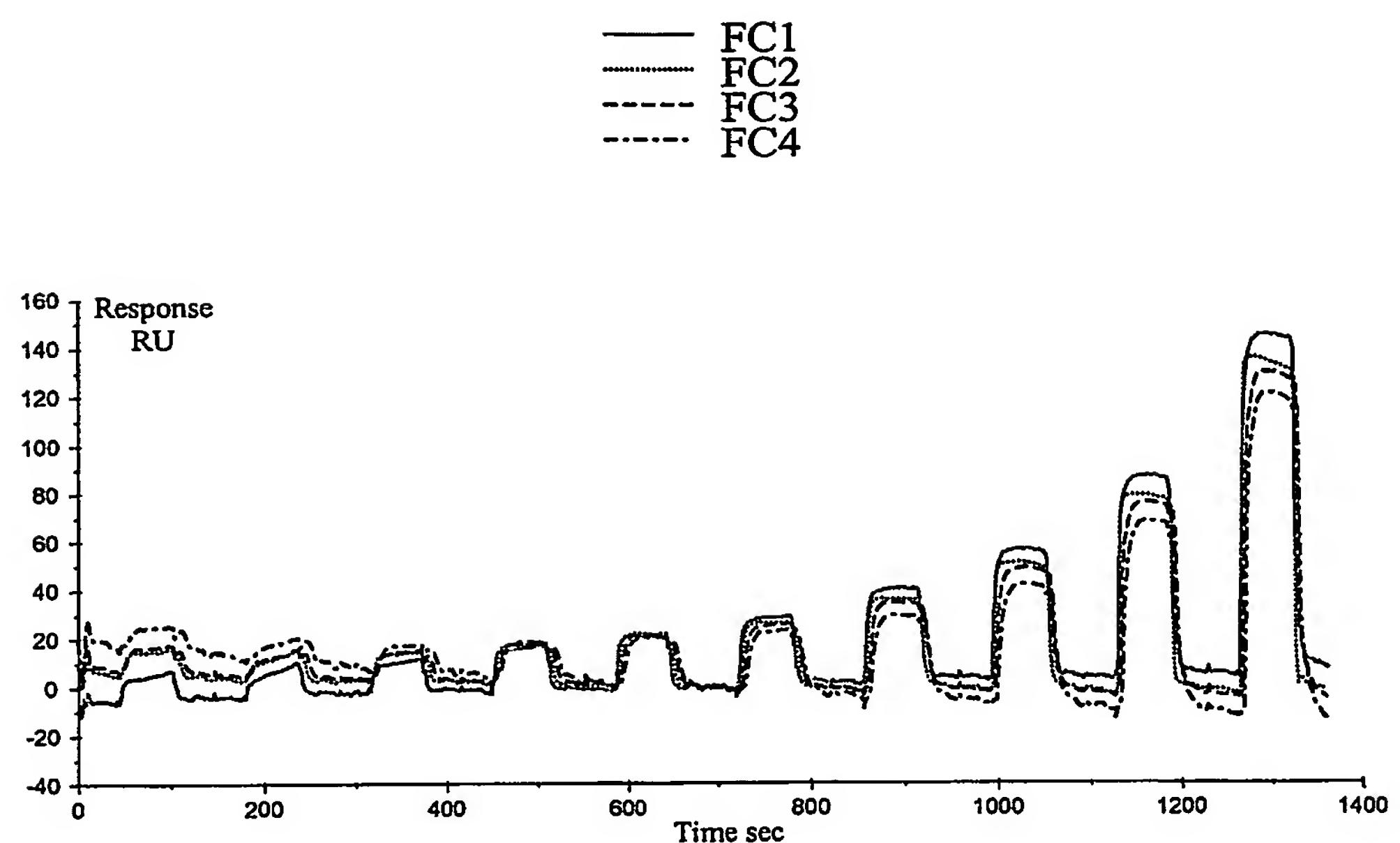
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**xxx**

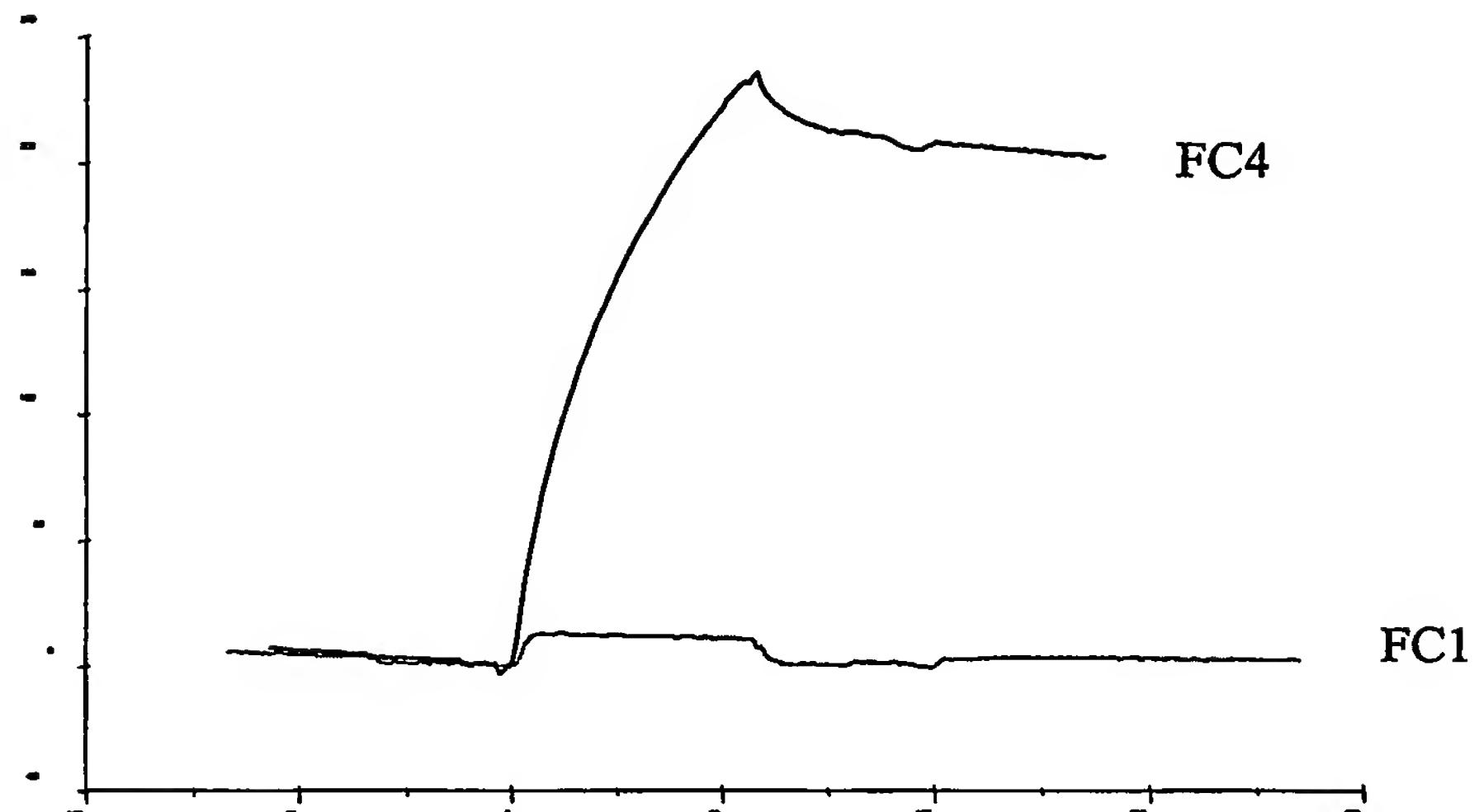
- Jun Leucine zipper codons  
- HLA-loaded peptide

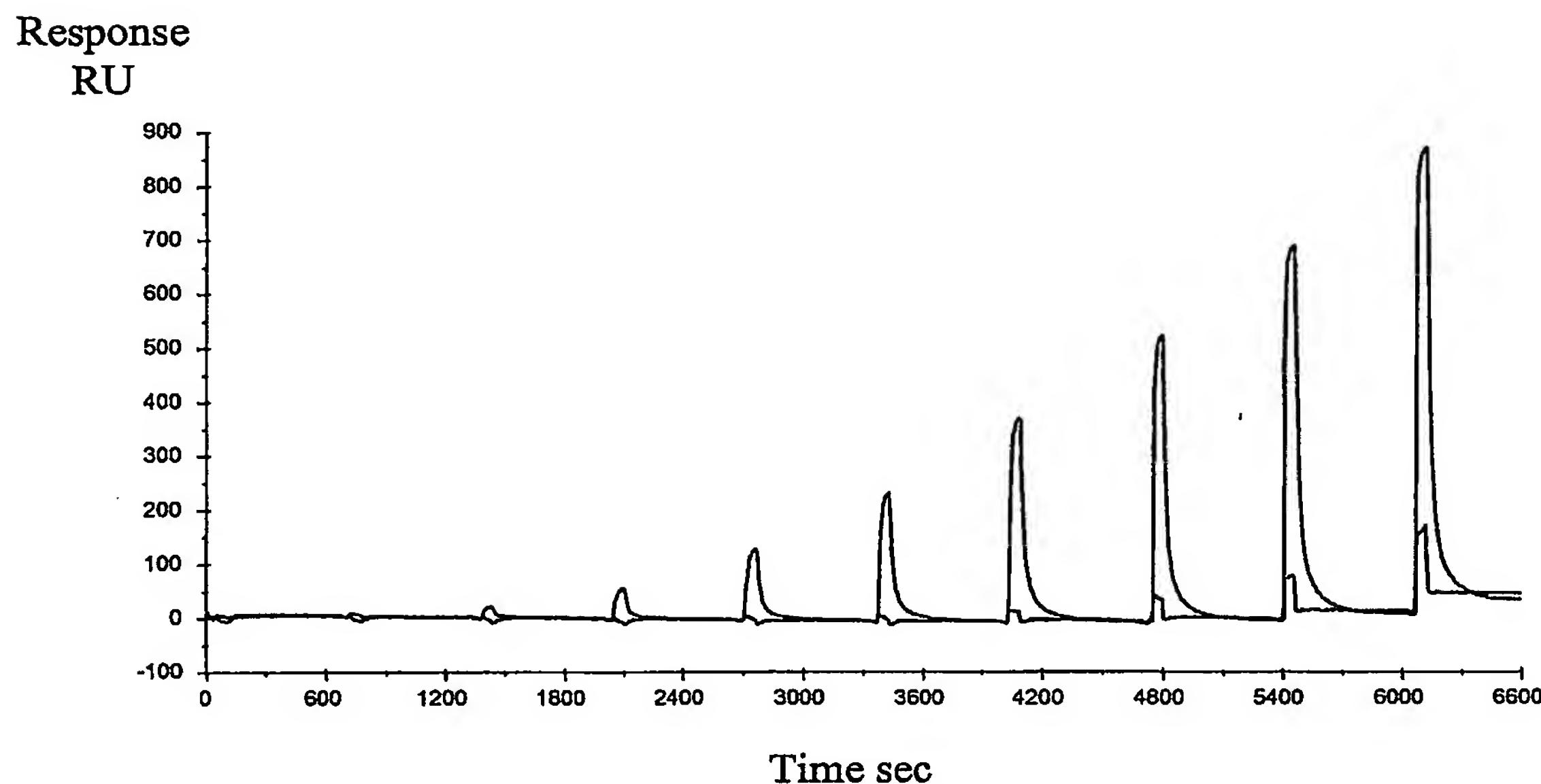
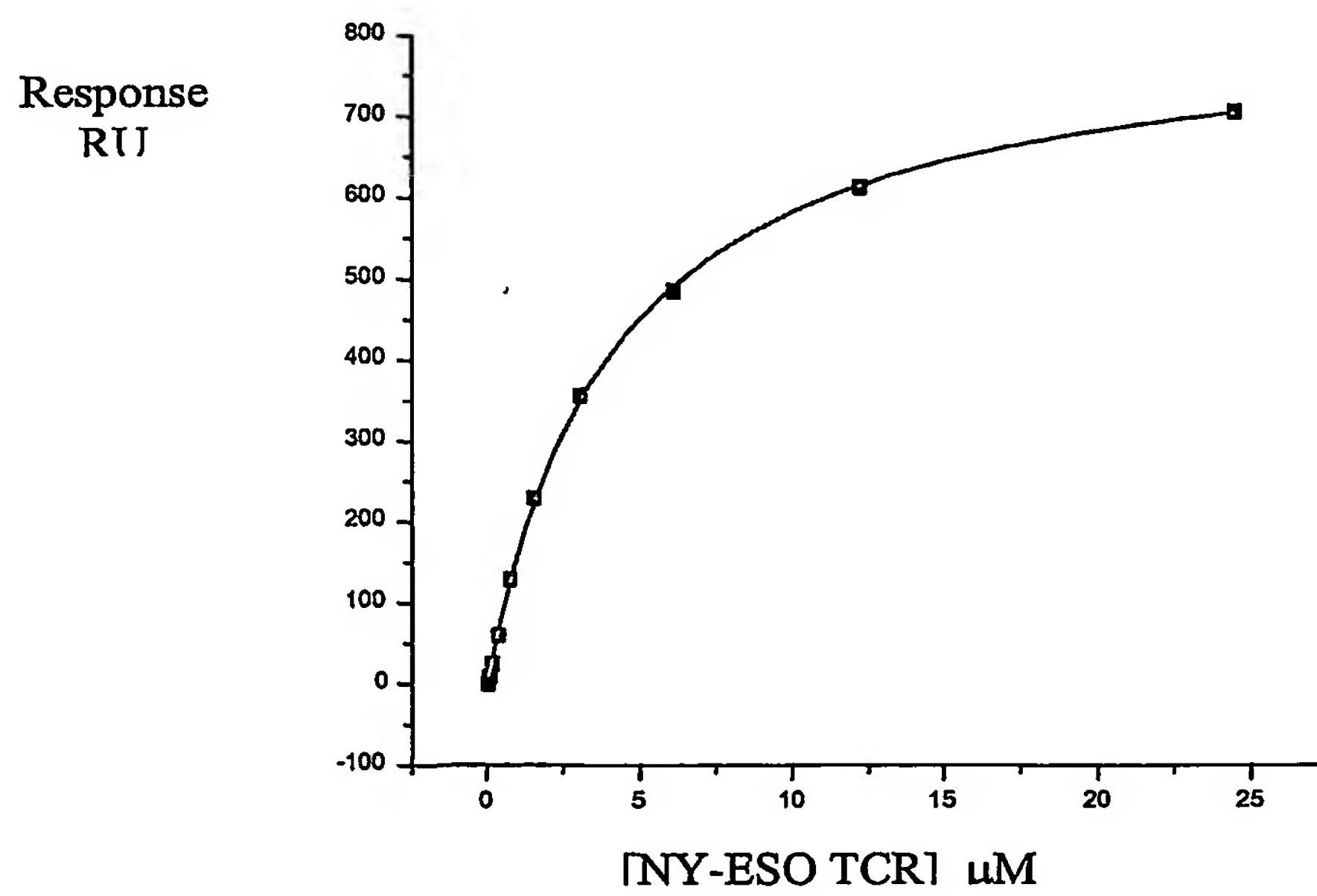
**Figure 24**

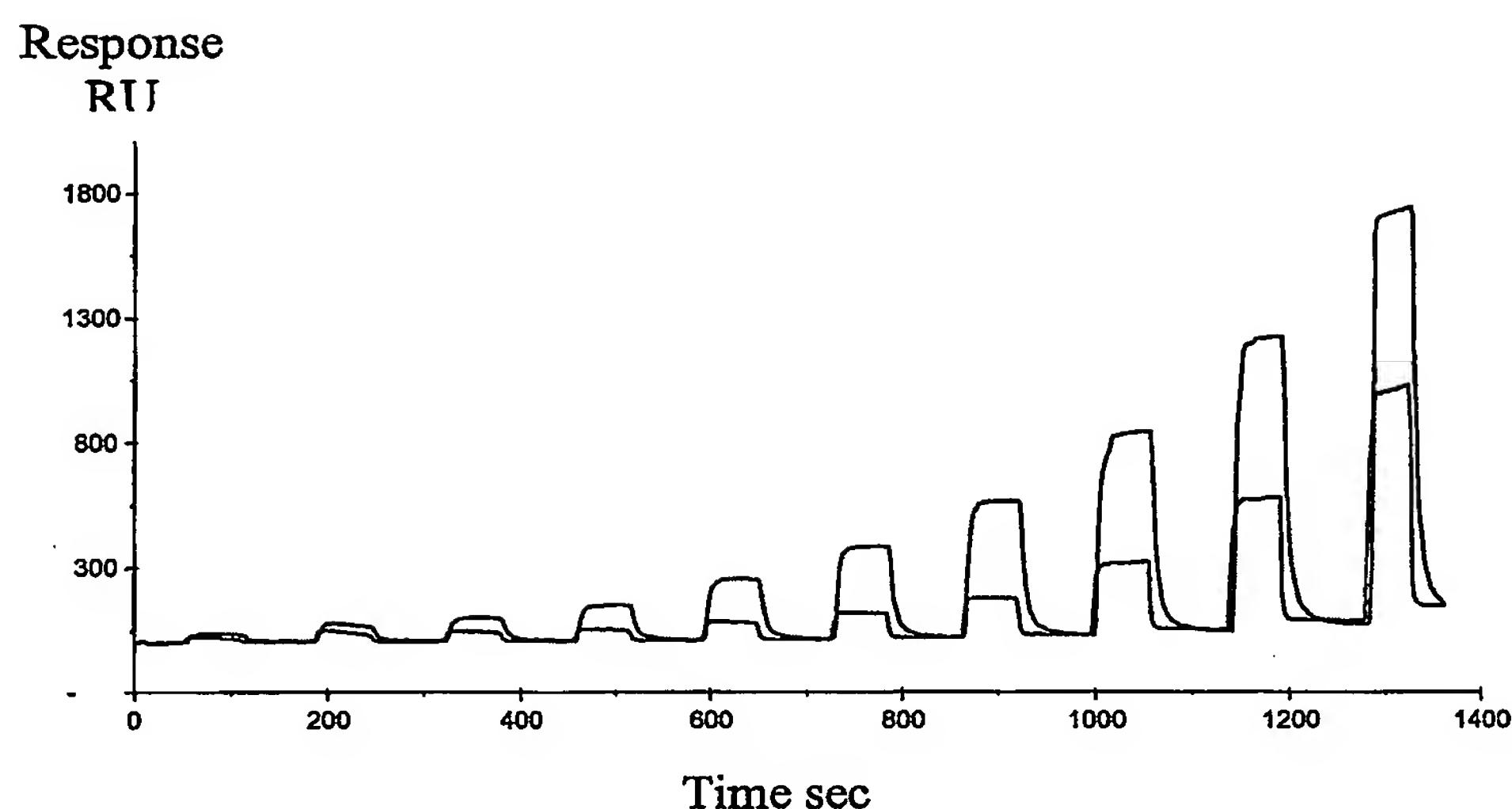
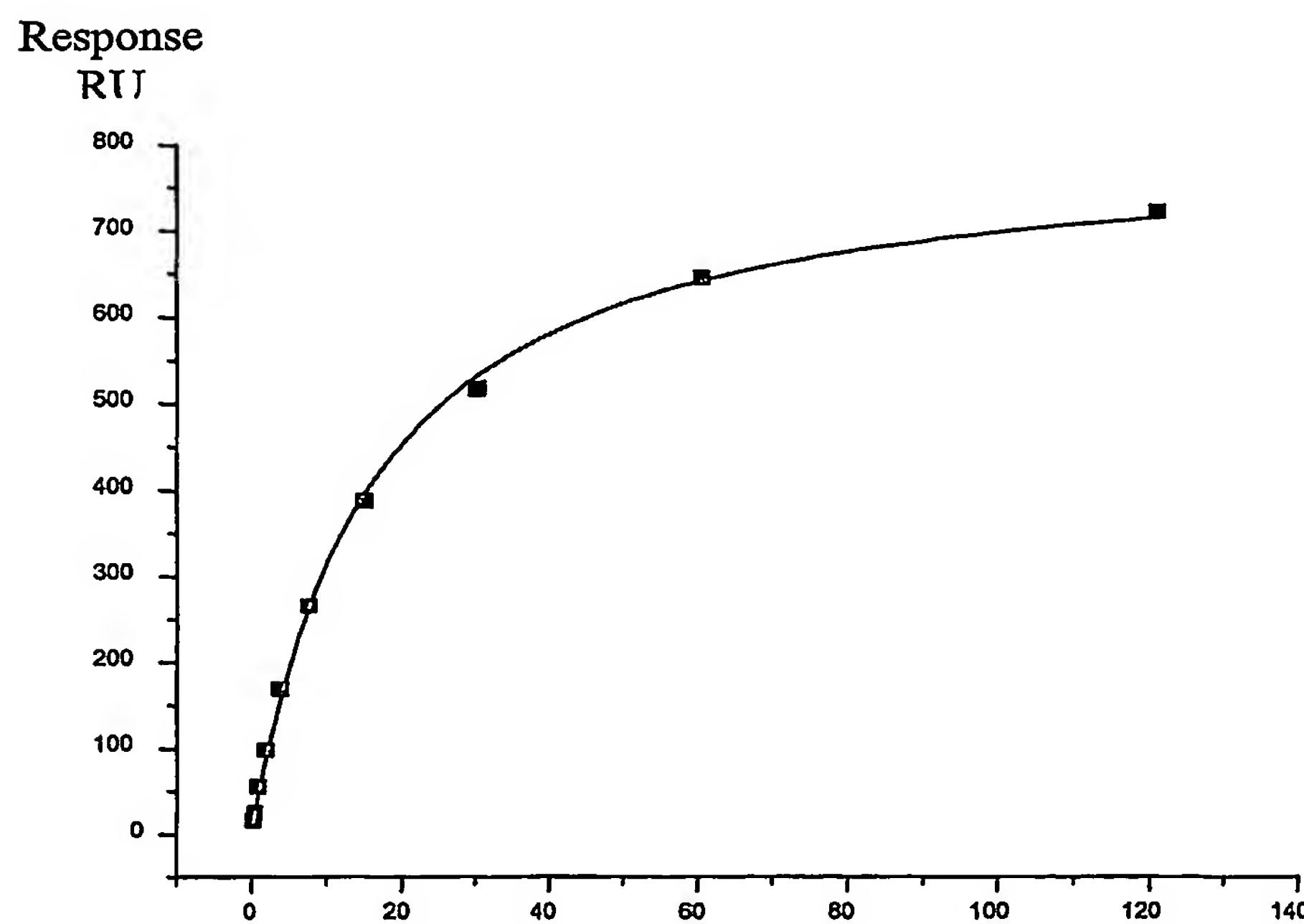
**Figure 25**

**Figure 26**

**Figure 27**

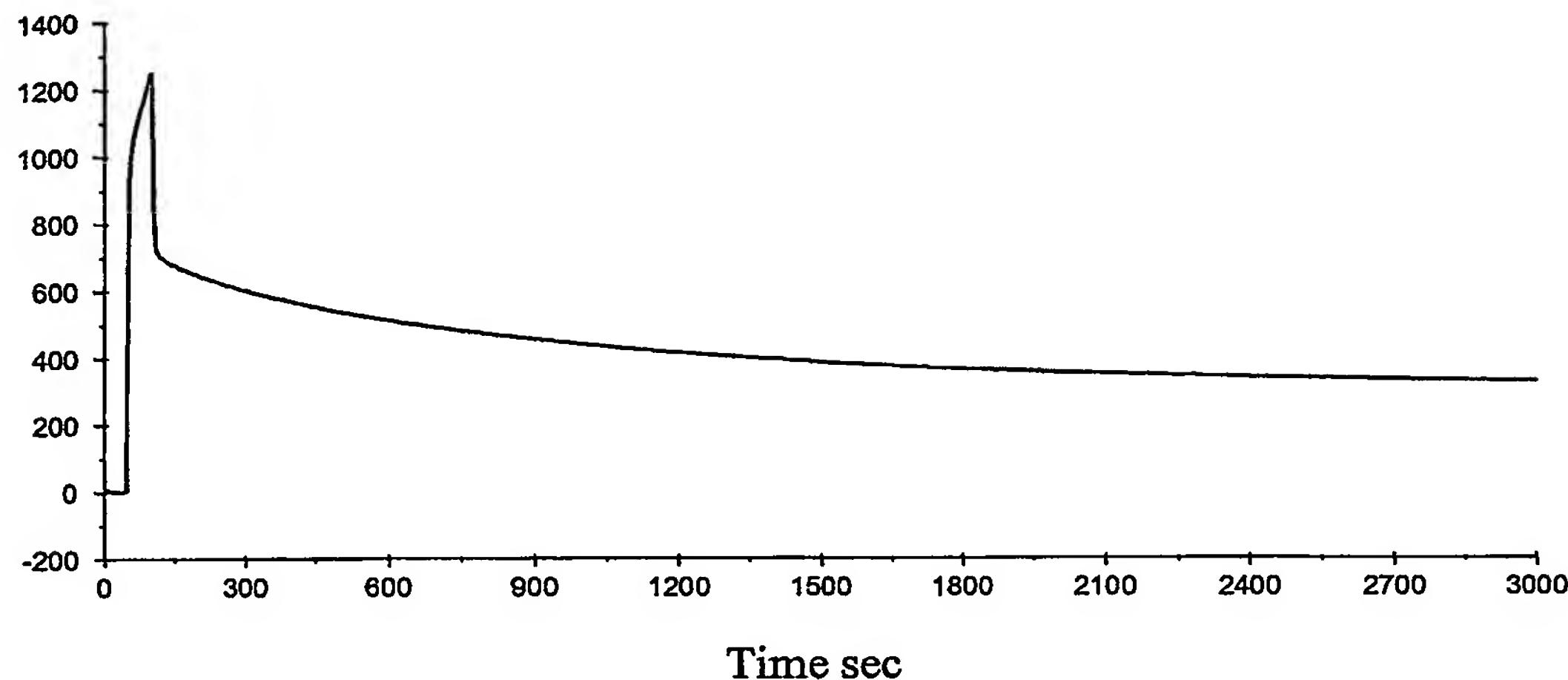
**Figure 28**

**Figure 29a****Figure 29b**

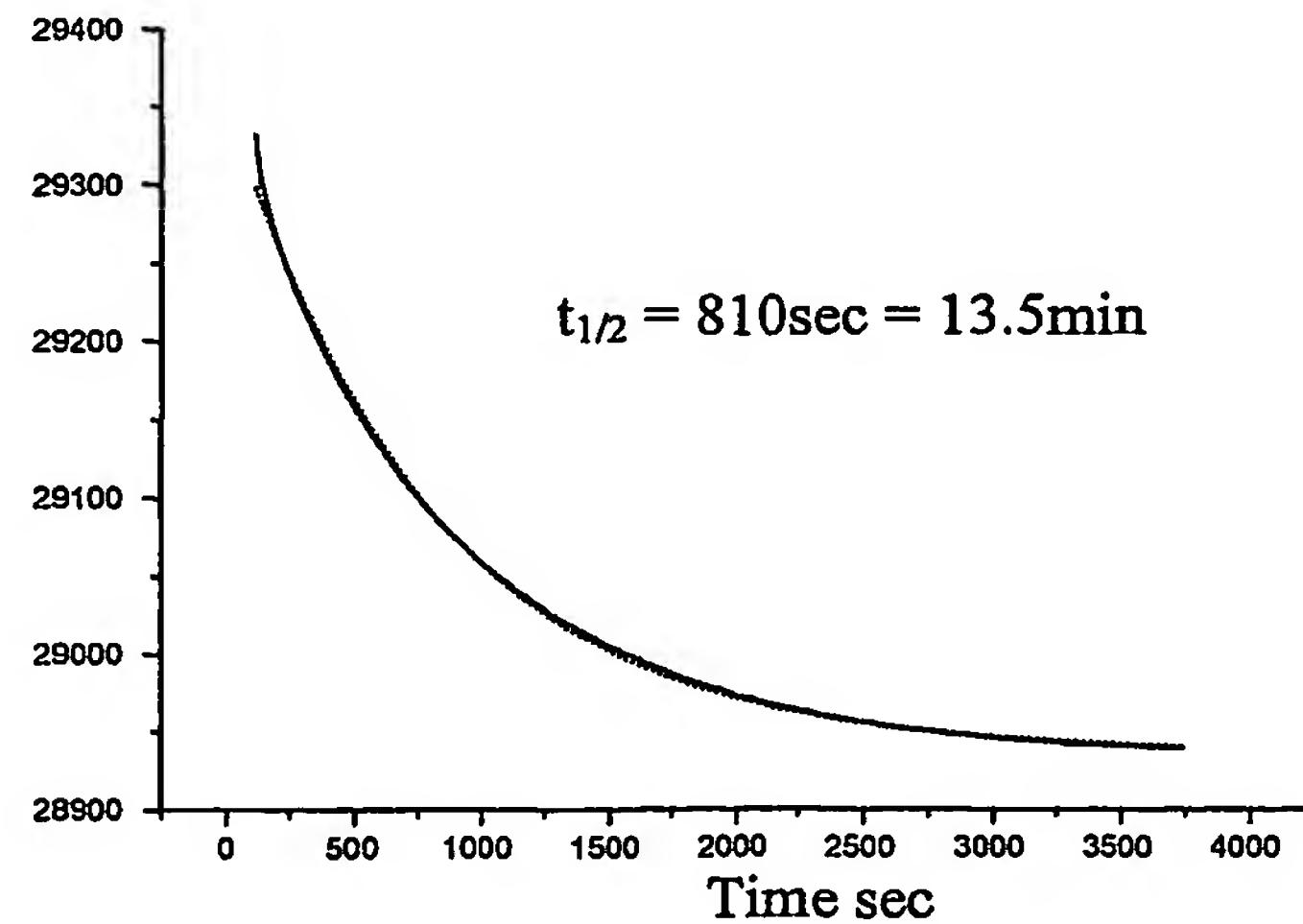
**Figure 30a****Figure 30b**

**Figure 31a**

Response RU

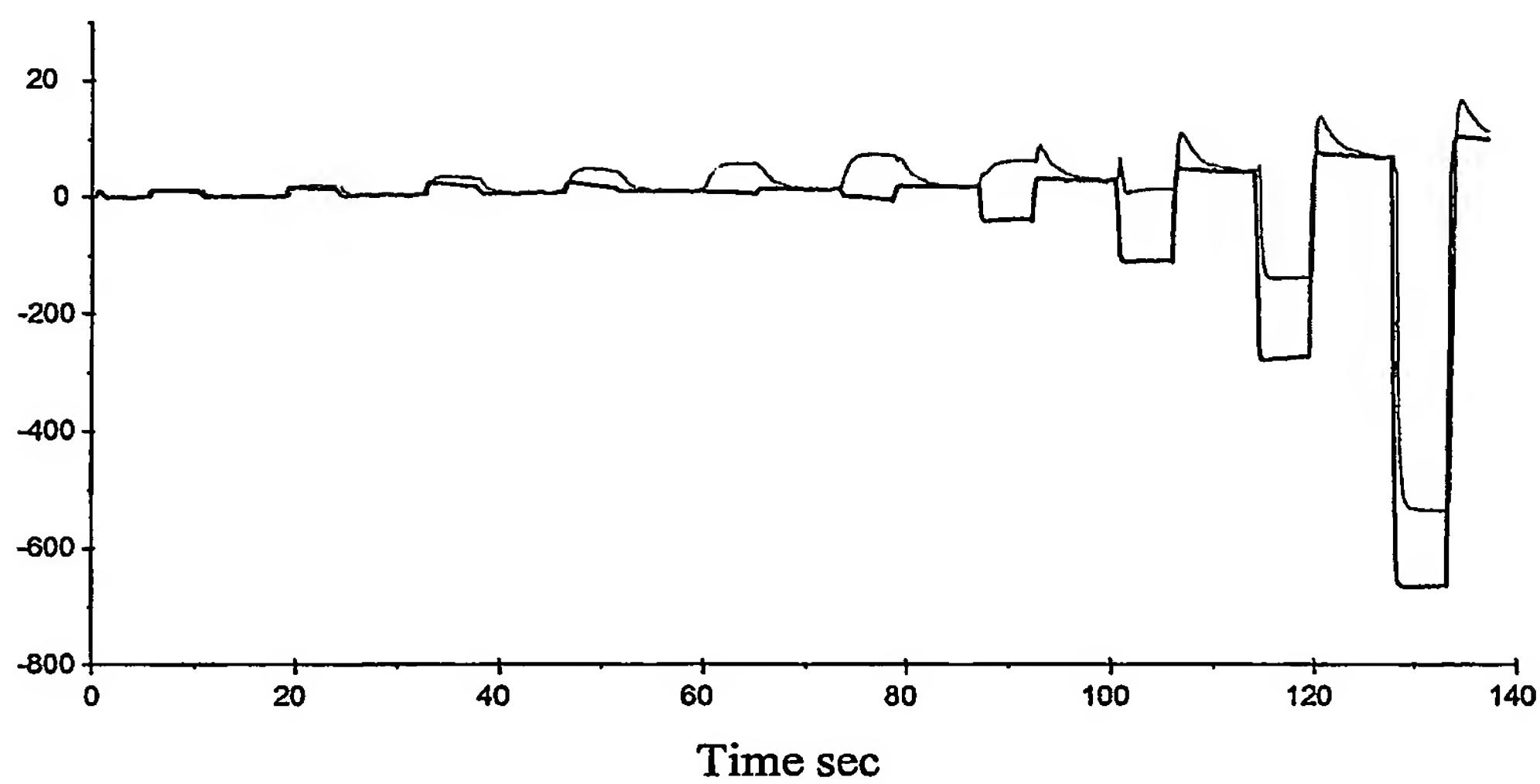
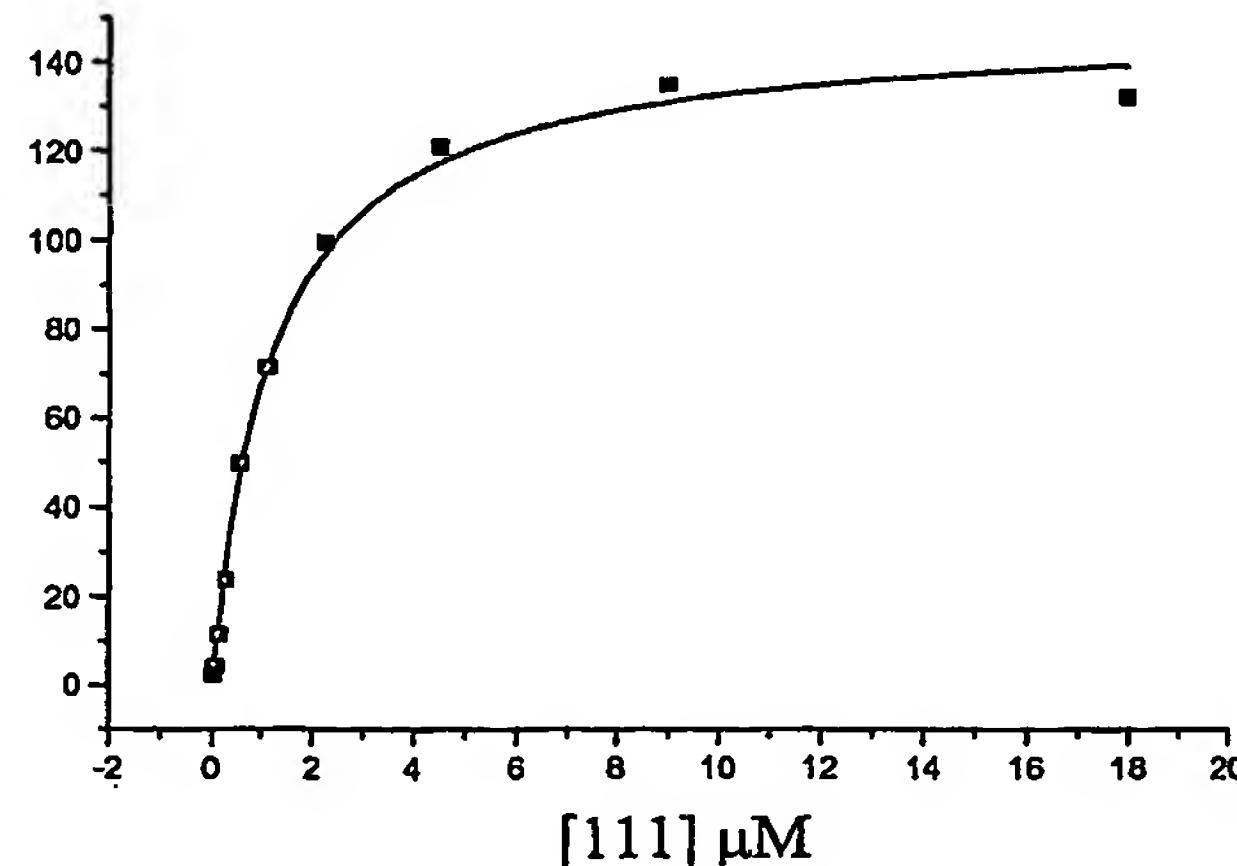
**Figure 31b**

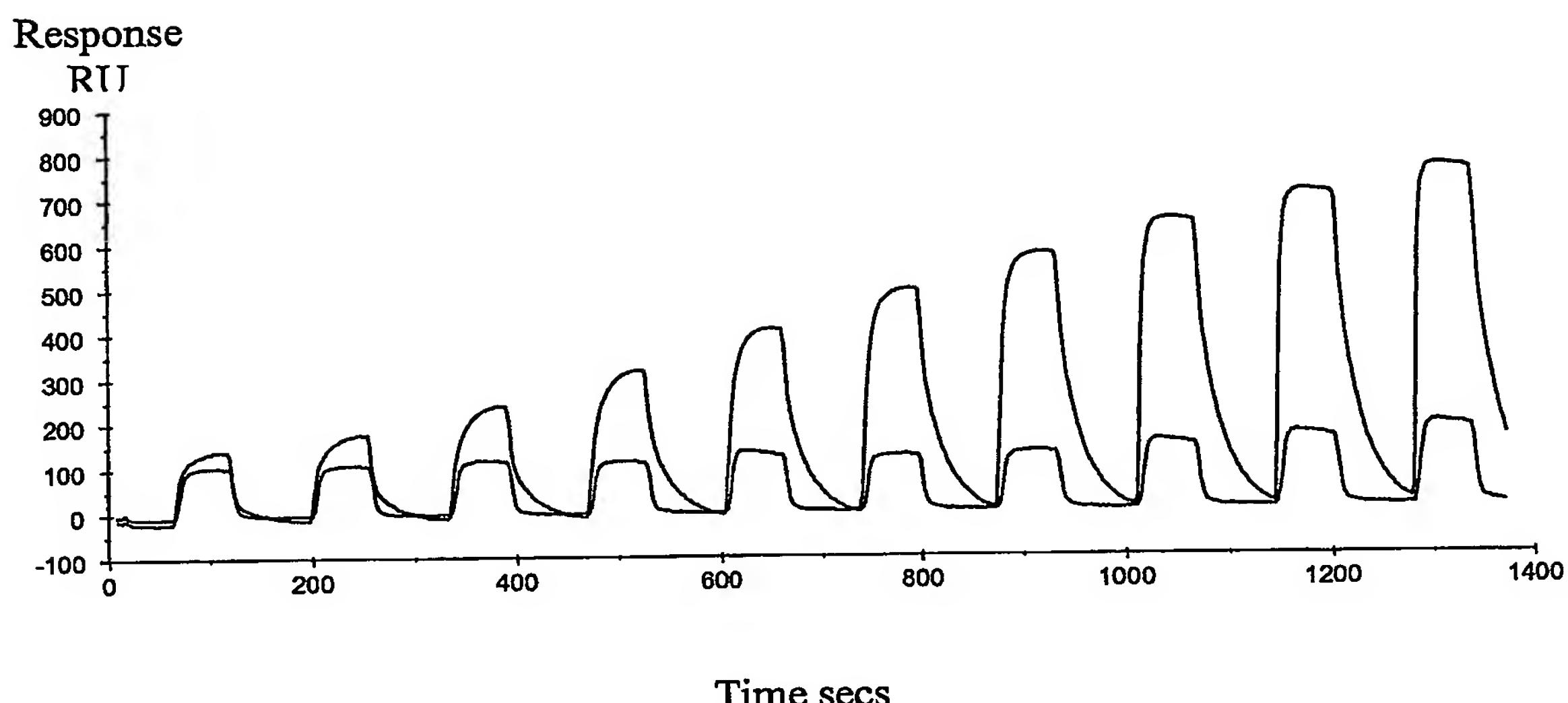
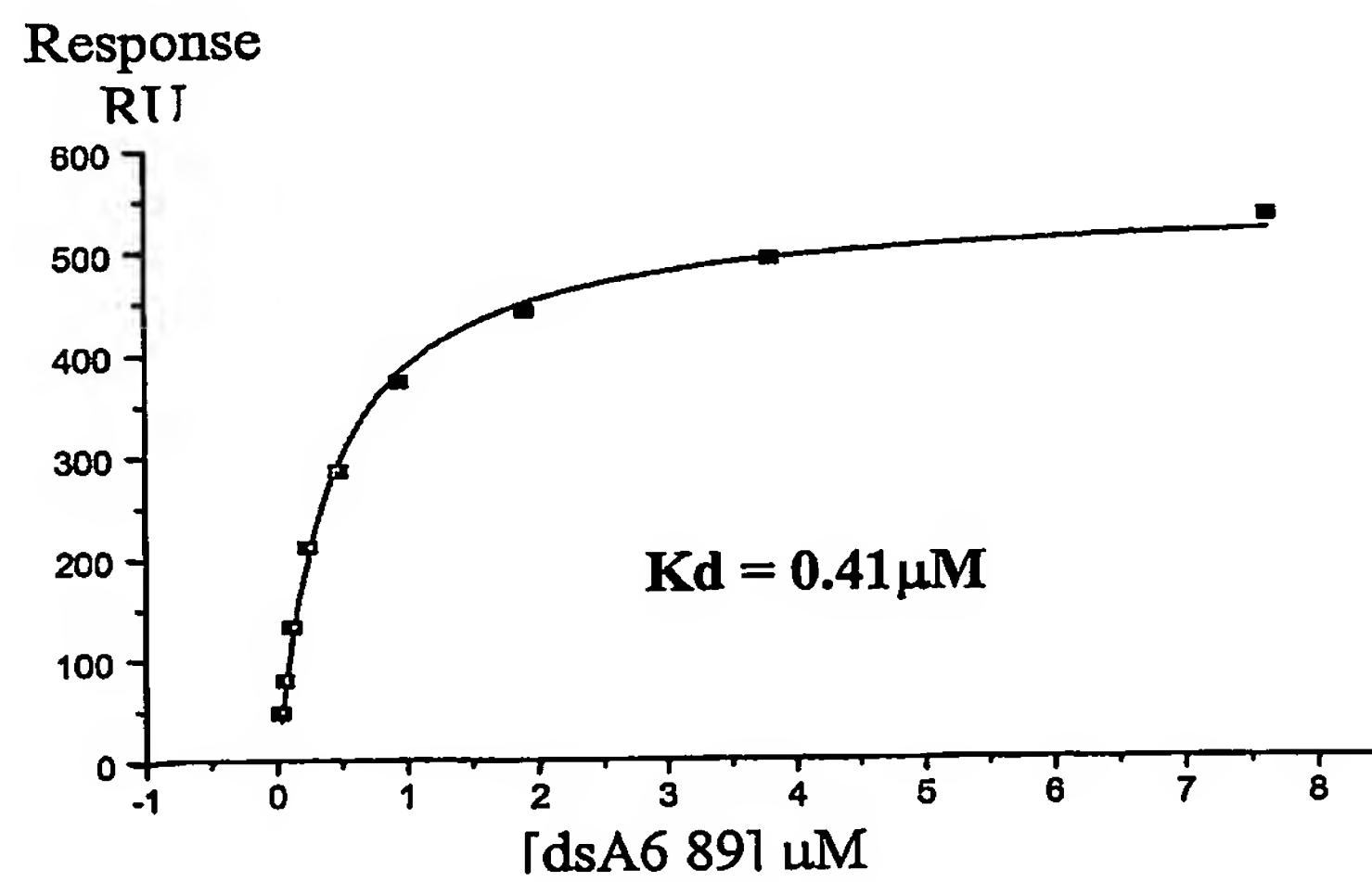
Response RTJ

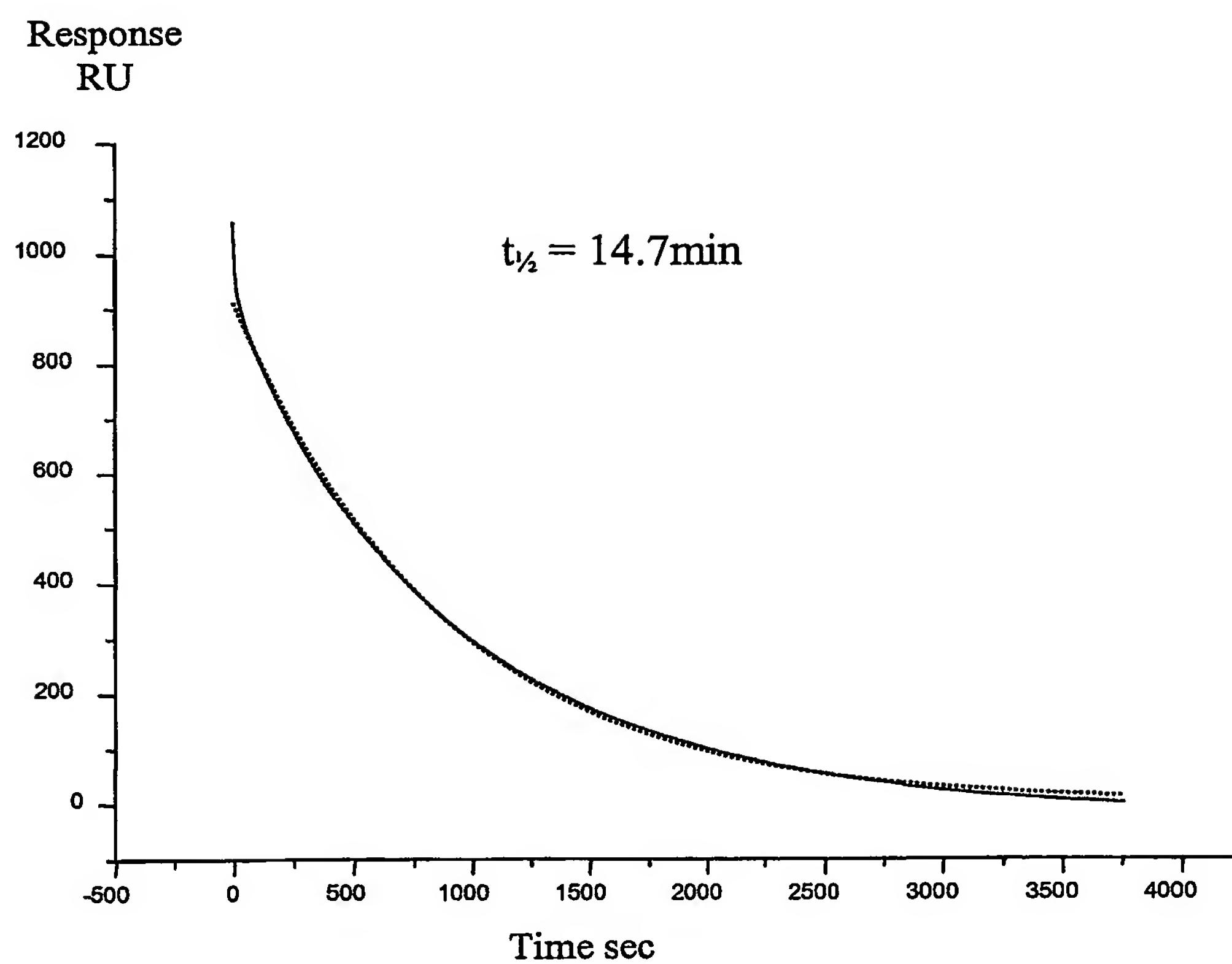


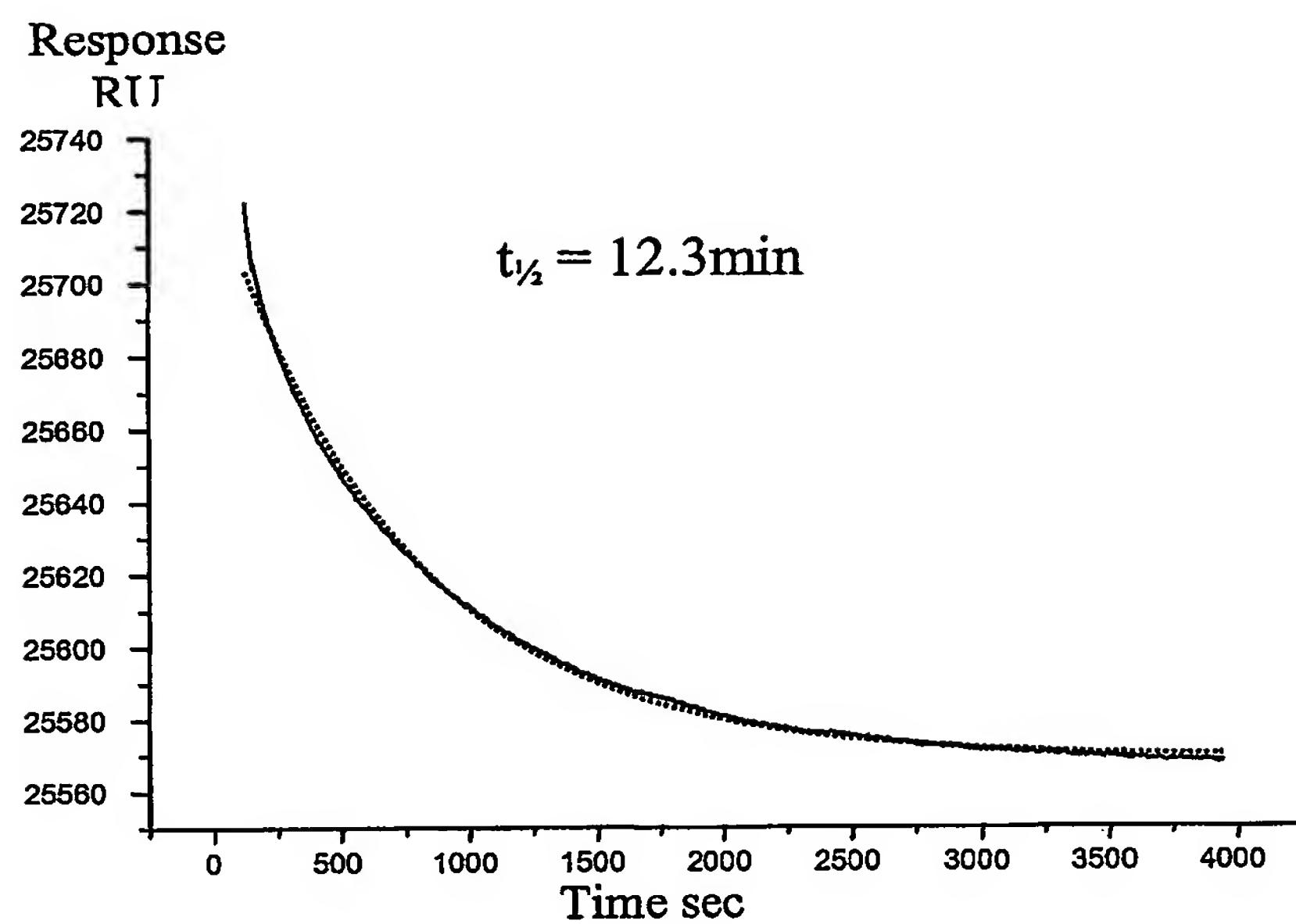
**Figure 32a**

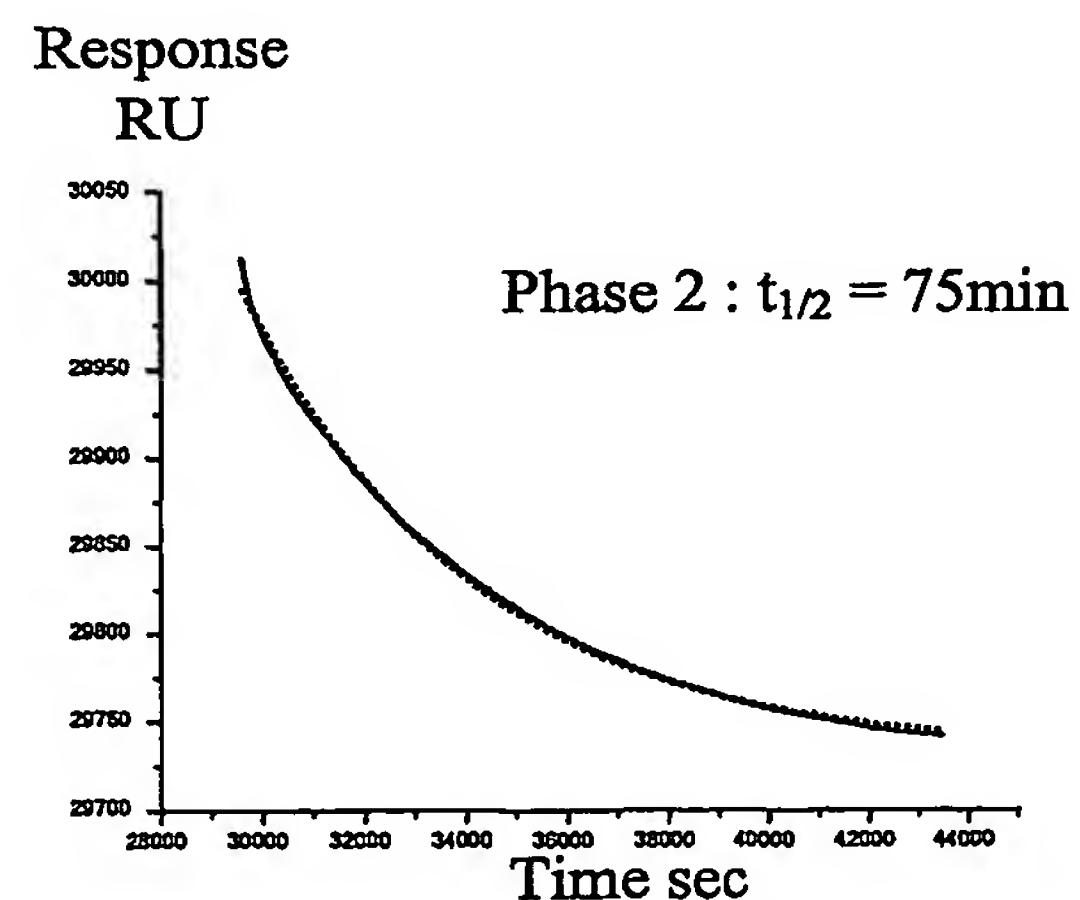
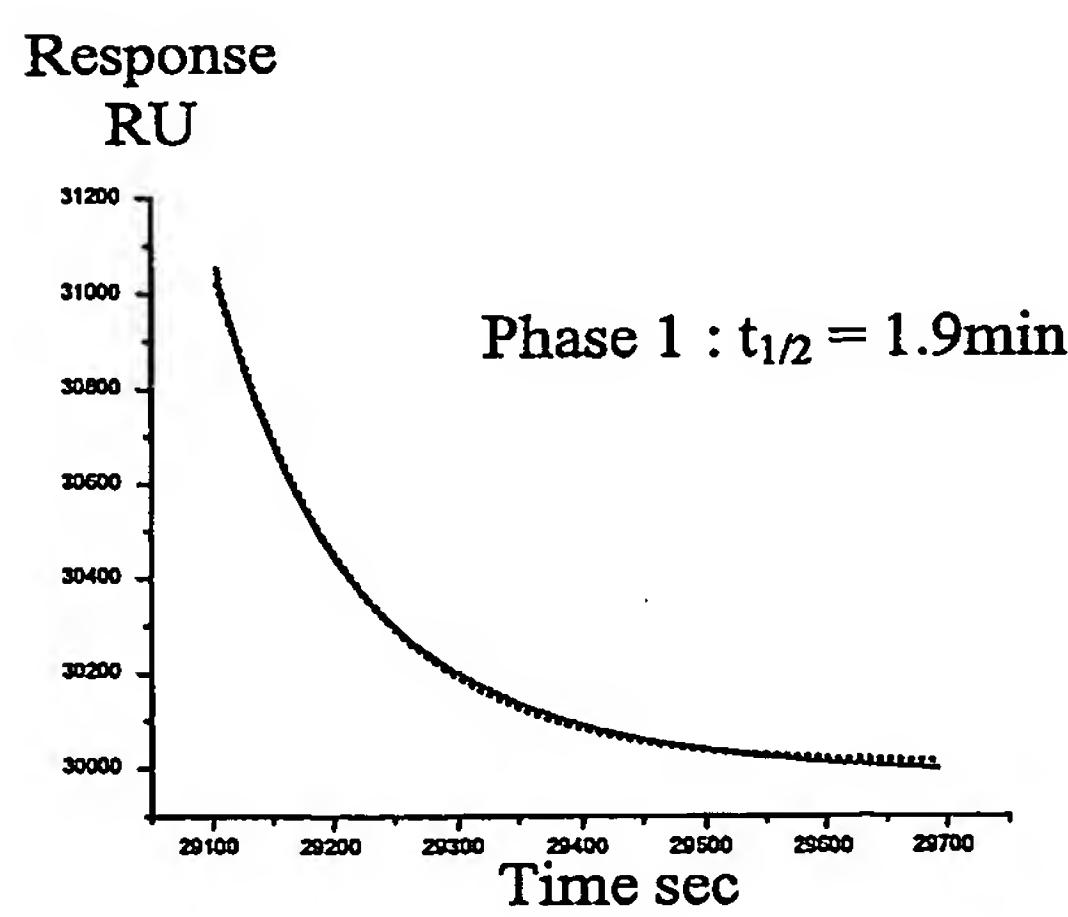
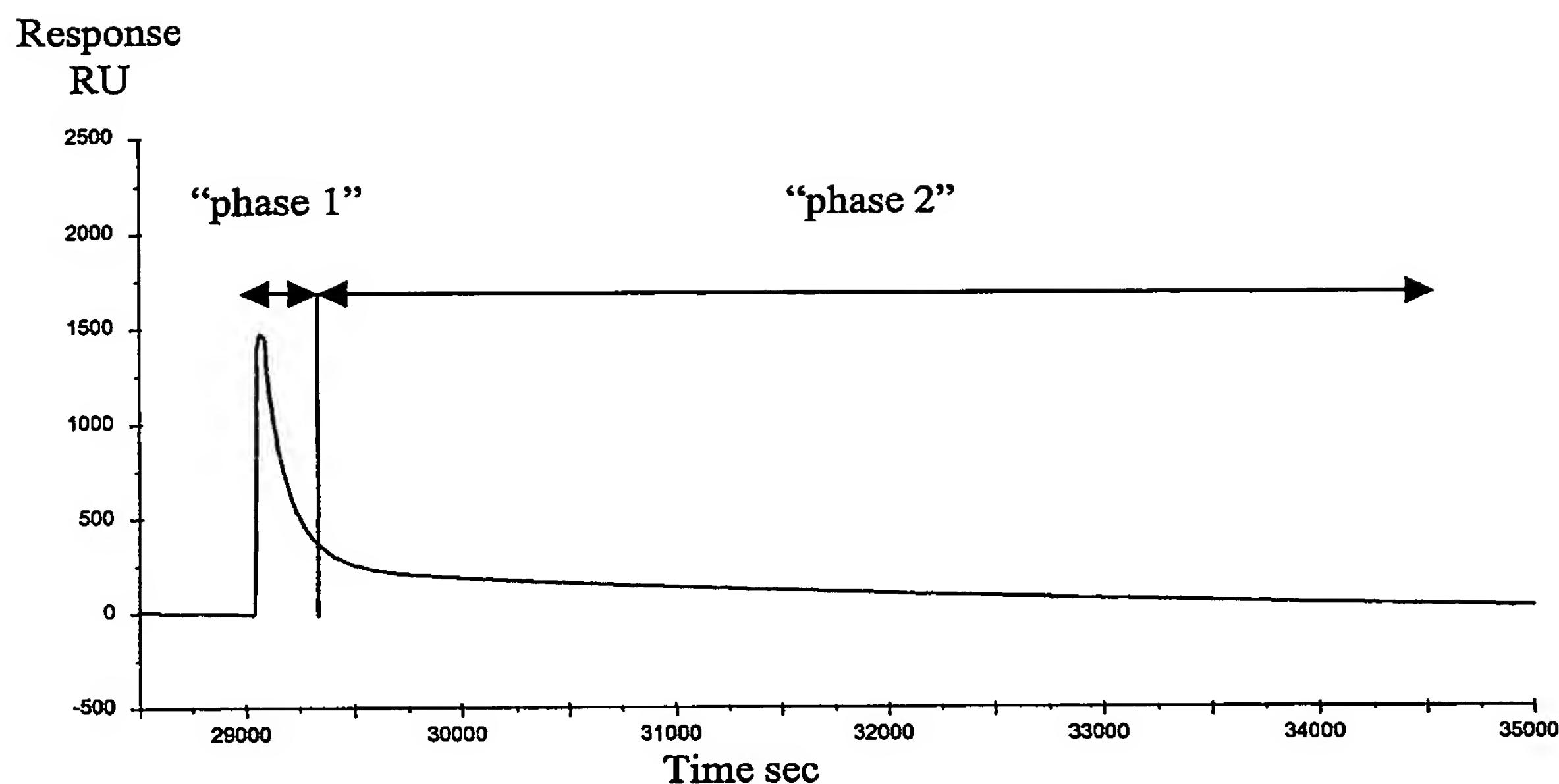
Response RU

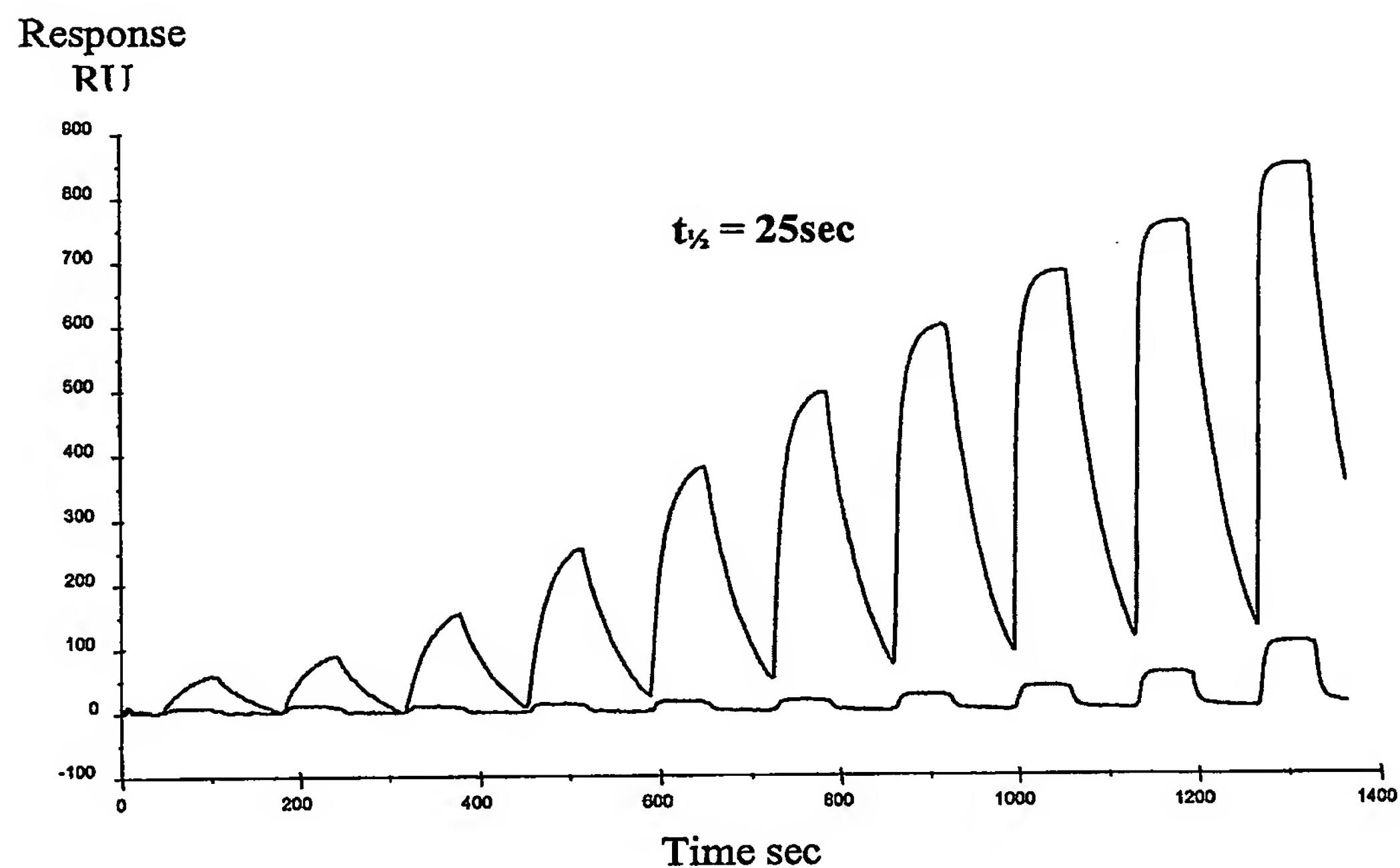
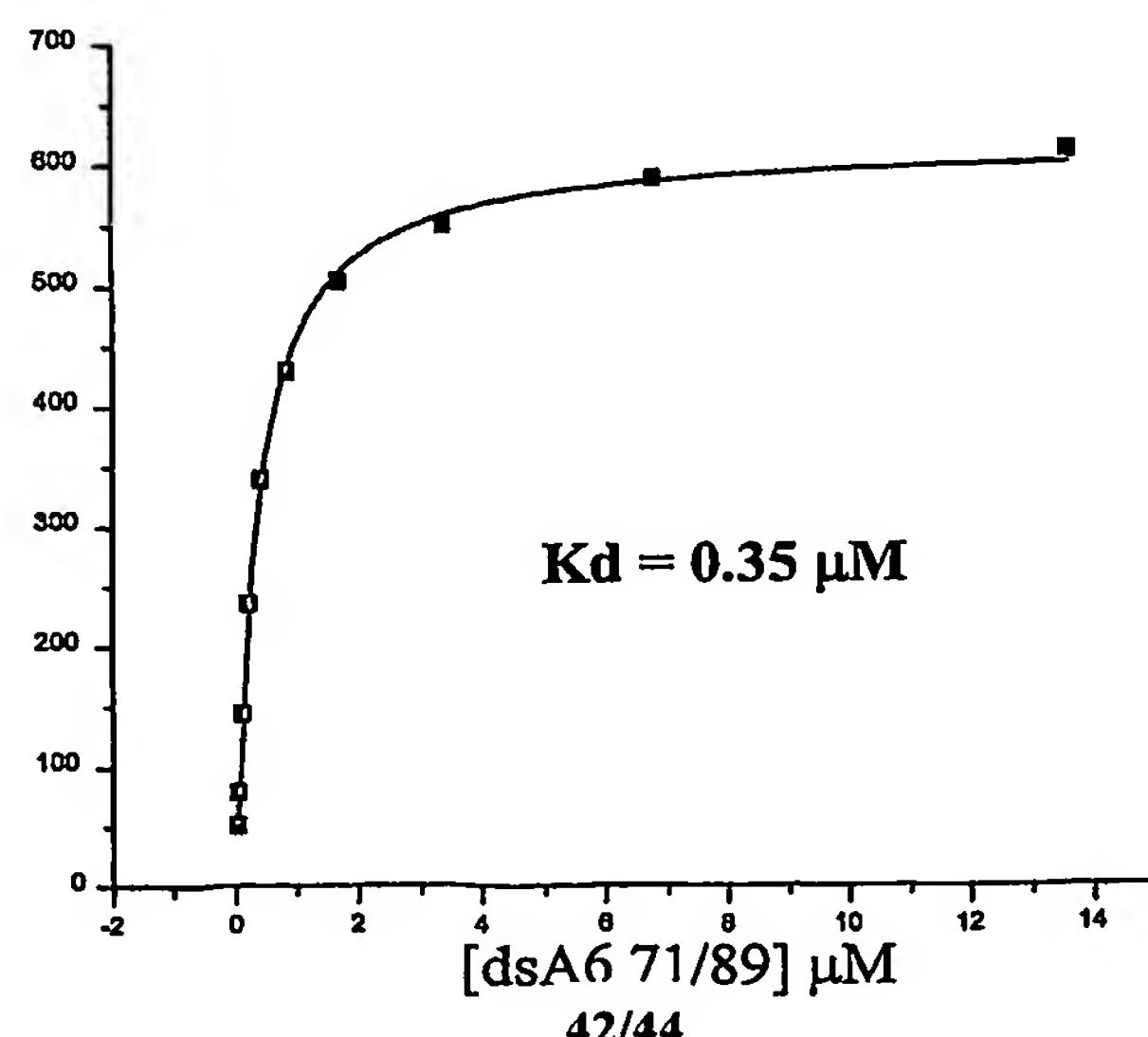
**Figure 32b**Response  
RU

**Figure 33a****Figure 33b**

**Figure 34**

**Figure 35**

**Figure 36**

**Figure 37a****Figure 37b**

**Figure 38a**

MNAGVTQTPKF QVLKTGQSMT LQCAQDMNHE YMSWYRQDPG  
MGLRLIHYSV GAGITDQGEV PNGYNVSRST TEDFPLRLLS AAPSQTSVYF  
CASRPGLAGG RPEQYFGPGT RLTVT (SEQ ID 171)

**Figure 38b**

MNAGVTQTPKF QVLKTGQSMT LQCAQDMNHE YMSWYRQDPG  
MGLRLIHYSV GAGITDQGEV PNGYNVSRST TEDFPLRLLS AAPSQTSVYF  
CASRPGLMSAXPEQYFGPGT RLTVT (SEQ ID 172)

X denotes a position at which amino acids E, Q or R can be inserted.

**Figure 38c**

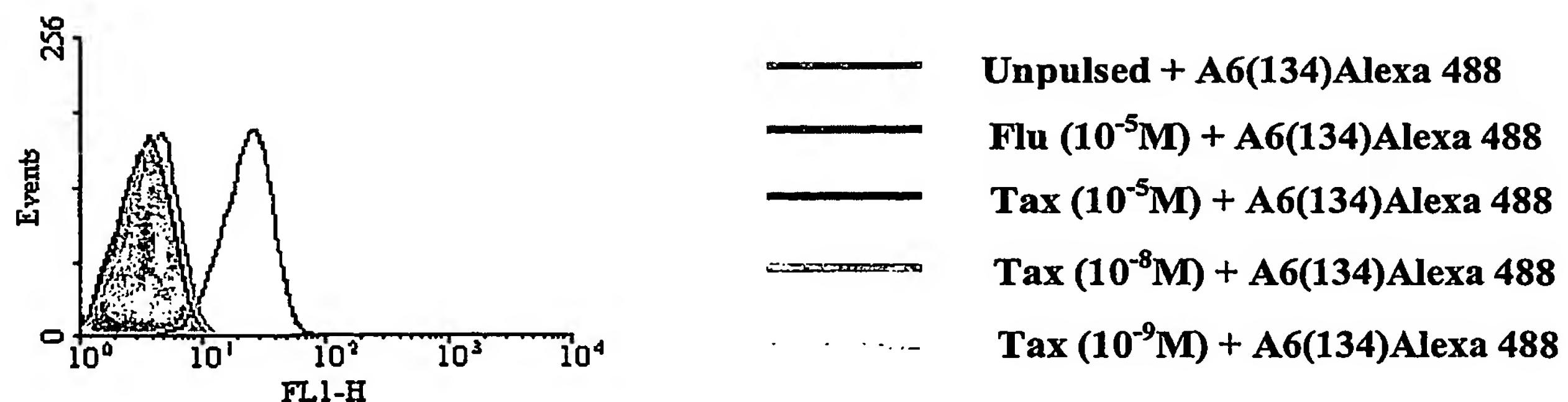
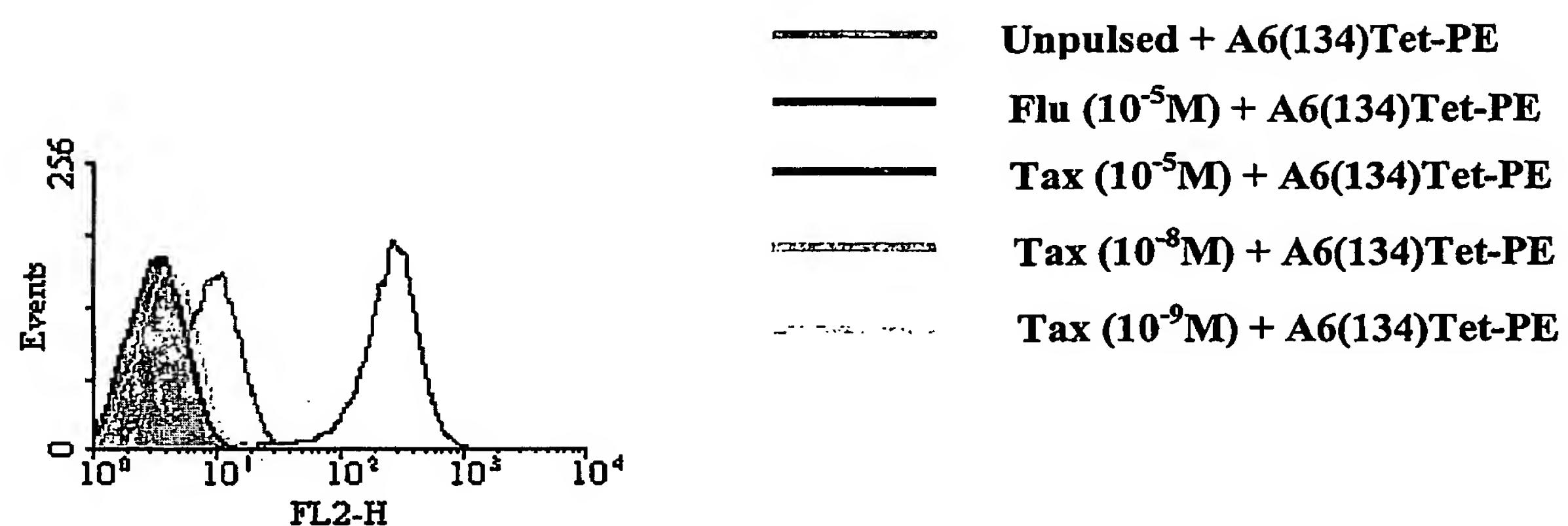
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MGLRLIHYSV GAGITDQGEV PNGYNVSRST TEDFPLRLLS AAPSQTSVYF  
CASRPGLAGG RPEDQYFGPGT RLTVT (SEQ ID 173)

**Figure 38d**

MNAGVTQTPKF QVLKTGQSMT LQCAQDMNHE YMSWYRQDPG  
MGLRLIHYSV GAGITDQGEV PNGYNVSRST TEDFPLRLLS AAPSQTSVYF  
CASRPGLVPG RPEQQFGPGT RLTVT (SEQ ID 174)

**Figure 38e**

MNAGVTQTPKF QVLKTGQSMT LQCAQDMNHE YMSWYRQDPG  
MGLRLIHYSV GAGITDQGEV PNGYNVSRST TEDFPLRLLS AAPSQTSVYF  
CASRPGLAGG RPHPQFGPGT RLTVT (SEQ ID 175)

**Figure 39a****Figure 39b**